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(54) Title: **PROTEIN KINASES**

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

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DESCRIPTION
PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple alignment of the sequences in the catalytic domain of protein kinases and subsequent
20 parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

10 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

25 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting

SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides
conjugated to each other, including DNA and RNA, that is isolated from a natural source
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"
indicates that a naturally occurring sequence has been removed from its normal cellular
(*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or
placed in a different cellular environment. The term does not imply that the sequence is
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at
least) of non-nucleotide material naturally associated with it, and thus is distinguished
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of
20 the total DNA or RNA present in the cells or solution of interest than in normal or
diseased cells or in the cells from which the sequence was taken. This could be caused by
a person by preferential reduction in the amount of other DNA or RNA present, or by a
preferential increase in the amount of the specific DNA or RNA sequence, or by a
combination of the two. However, it should be noted that enriched does not imply that
25 there are no other DNA or RNA sequences present, just that the relative amount of the
sequence of interest has been significantly increased. The term "significant" is used to
indicate that the level of increase is useful to the person making such an increase, and
generally means an increase relative to other nucleic acids of about at least 2 fold, more
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The other source DNA may, for example, comprise
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

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NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%
15 and most preferably 99-100%) to a sequence selected from the group consisting of those
set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ
ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ
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By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
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NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
5 NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
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NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
10 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most
preferably 99-100%) to the sequence selected from the group consisting of those set forth
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
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NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
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NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
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5 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
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NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
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NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
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NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
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NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
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NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the
group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a
coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-
terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a
polypeptide having an amino acid sequence selected from the group consisting of those set
30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
5 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
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NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
10 NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
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NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
15 NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%
and most preferably 99-100%) to the sequence selected from the group consisting of those
20 set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ
ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ
ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ
ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ
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ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ
ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ
ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ
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ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ
ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of

those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, 5 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, 10 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, 15 SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, 20 SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, 25 SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, 30 a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID
NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID
NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID
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NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID
NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID
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NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID
NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
25 NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino
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SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
30 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
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SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
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5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
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SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
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NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
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NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
30 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
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NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
5 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
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20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
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25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
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NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
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NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_o subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).
5 Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of
10 the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein
15 database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these
20 methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the
25 protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of
30 the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

5 The term “vector” relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding
10 a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term “transfecting” defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field,
15 detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term “promoter” as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes,
20 the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

25 In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19,
30 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID
NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51,
SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ
5 ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID
NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67,
SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ
ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID
NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83,
10 SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ
ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID
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SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
15 SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114,
SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119,
SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes
an amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
20 NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.

25 In particular, a unique nucleic acid region is preferably of mammalian origin and preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
5 NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
10 NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the
corresponding full-length amino acid sequence. By "fragment," is meant an amino acid
sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least
10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the
group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
15 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
20 SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
25 SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
30 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (e.g., in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, 10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, 15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, 20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, 25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, 30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it
lacks one or more, but not all, of the domains selected from the group consisting of a C-
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The
isolated, enriched, or purified kinase polypeptide is preferably selected from the group
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By “recombinant kinase polypeptide” is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By “specific binding affinity” is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term “specific binding affinity” describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term “polyclonal” refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

“Monoclonal antibodies” are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term “antibody fragment” refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID

NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term "modulates" refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term “complex” refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term “natural binding partner” refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term “contacting” as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
10 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
15 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term “expressing” as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term “preventing” refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term “treating” refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

The term “therapeutic effect” refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of
10 abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating
15 efficacy against abnormal conditions can be identified as described herein.

The term “abnormal condition” refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in
20 normal cell cycle progression through mitosis and meiosis.

Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

Abnormal differentiation conditions include, but are not limited to
25 neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the
30 protein kinases could lead to cell immortality or premature cell death.

The term “aberration”, in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term “administering” relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding

full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

“Amplification” as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
20 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
25 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
30 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include, but are not limited to, those discussed previously.

The term “comparing” as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine these discrepancies in sequences are well-known to one of ordinary skill in the art. The “control” nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide or polynucleotide may be used in this regard, provided that its addition, deletion or substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

5 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

10 If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

20 Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiol. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any
5 organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

10 Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

15 One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that
20 can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
25 SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,
30 SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
 SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
 SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
 5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
 SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant
 number of protein kinases that do not belong to any of the known groups, and therefore
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,
 Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein 25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of
 the invention. The polypeptide may have an amino acid sequence selected from the group
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspiczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5 Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15 Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20 Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

25 Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

30 A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic
25 acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express
5 a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid
10 sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or
15 modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

20 X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by
25 reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of
30 the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

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Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

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Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

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with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATTT TGAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 – Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

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PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the *evc* (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceded by the sequence "RGLLAPGDPPCPPNPAPATPPSSRLPTELF SNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2 , Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

15 Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

25 Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNNGEGHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRRGKKVNMALGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence 1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). “Kinase Domain Start”, “Kinase Domain End”, “Profile Start” and “Profile End” refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a “Profile Start” of 1 and a “Profile End” of 261. The boundaries of the catalytic domain within the overall protein are noted in the “Kinase Domain Start” and “Kinase Domain End” columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca ²⁺ /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQKGDKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon
5 membranes and probed with ³²P-labeled cDNA fragments derived from the gene(s) of
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at
each end. An oligo dT primer containing a specific sequence (CDS:

10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when
it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”
A double-stranded “cDNA library “ is then generated by PCR amplification using the
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)
and hybridized with ³²P labeled probes generated by random hexamer priming of cDNA
fragments corresponding to the genes of interest. After washing, the blots were exposed to
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: “Tissue”: tissue type of the cDNA; “Tumor sym”, indicates that the tissue is derived from a tumor, “sym” refers to the fact that the 5’ and 3’ primers used to make the sample are the same; “Normal Sym”, indicates normal tissue was used to make the sample, with symmetric primers as described above; “Tumor 1o”, indicates that primary tumor tissue was used to make the cDNA; “Tumor cells”, indicates that these cDNA samples were made from cultured tumor cells; “Normal”, indicates that these samples are derived from normal tissue or cell lines; “Endos”, indicates that these samples are derived from endothelium-related tissue sources; “p53” refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. ... An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
5 NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
10 NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
15 NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
20 NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
25 NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

30 (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
10 SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
15 SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
20 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
25 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
30 and SEQ ID NO:242.

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
5 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
10 NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
15 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
20 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
25 NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
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ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

5 ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
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ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
10 ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
15 ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from
the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a
spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set
20 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
25 NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
30 NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ

ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said

polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

5 NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
10 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
15 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
20 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) adding a test substance to said cell; and

(c) monitoring a change in cell phenotype or the interaction between
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

(b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

Gen Name	SP	Pro Seq ID NA	Pro Seq ID AA	SEQ ID # na	SEQ ID # aa	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeats	CHR Localization
XG9117 h BARK2 h	H	1	1	122	122	AGC	GRK	287	669	1	2054	2054	x	22q11
AA144574 m BARK2 m	M	1	17	123	123	AGC	GRK	1368	318	2	1135	1134	x	NA
AA208850 h	H	140	176	124	124	AGC	M3C11.1 ce	1768	419	8	1284	1237	285-304	NA
AA908057 h	H	1	27	125	125	AGC	M3C11.1 ce	3224	414	65	1306	1242	x	4p16.1
SG194541 h TBK1 h	H	207	208	5	126	AGC	M3C11.1 ce	3013	329	53	2278	2187	x	NA
AA305176 h	H	42	1820	127	127	AGC	NDR	582	88	3	1038	887	x	10p11.2
AA116841 m	M	42	1820	128	128	AGC	NDR	582	88	3	288	284	x	NA
AA238100 h	H	3	19	129	129	AGC	NDR	484	464	88	1477	1382	x	12q11
AA210825 h	H	5	21	130	130	AGC	PKC	323	315	117	3050	2934	x	18q13-q13.3
AA172799 h	H	203	204	131	131	AGC	PKC	2873	890	1	2870	2870	x	NA
AA316804 h EPK2	H	6	22	132	132	AGC	PKC	2870	889	1	2687	2687	2221-2280	NA
AA2050 h PKNbeta	H	8	24	133	133	AGC	PKC	2870	889	1	2687	2687	NA	NA
AA102131 m PKNbeta m	M	x	x	134	134	AGC	PKC	2870	889	1	2687	2687	NA	NA
AA102131 h	H	12	28	135	135	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h RPS6K1	H	0	25	136	136	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h RSK4	H	10	26	137	137	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	227	228	138	138	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	139	139	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 m	M	x	x	140	140	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 m	M	13	29	141	141	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h SGK3	H	16	32	142	142	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h SGK3	H	131	107	143	143	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	33	54	144	144	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	145	145	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	146	146	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	147	147	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	38	57	148	148	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	34	55	149	149	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	37	58	150	150	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	151	151	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	40	61	152	152	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	43	64	153	153	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	45	66	154	154	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	43	64	155	155	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	49	70	156	156	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	157	157	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	46	69	158	158	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	159	159	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	46	69	160	160	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	46	69	161	161	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	47	68	162	162	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	50	71	163	163	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	164	164	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	39	60	165	165	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	52	73	166	166	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	53	74	167	167	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	59	76	168	168	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	75	78	169	169	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	82	80	170	170	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	84	80	171	171	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	172	172	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	81	85	173	173	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	85	86	174	174	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	175	175	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	176	176	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	105	107	177	177	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	89	100	178	178	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	90	100	179	179	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	180	180	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	181	181	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	165	201	182	182	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	147	183	183	183	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	122	126	184	184	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	185	185	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	186	186	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	187	187	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	188	188	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	189	189	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	190	190	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	191	191	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	192	192	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	193	193	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	194	194	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	195	195	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	196	196	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	197	197	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	198	198	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	199	199	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	200	200	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	201	201	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	202	202	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	203	203	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	204	204	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	205	205	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	206	206	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	207	207	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	208	208	AGC	SGK	2870	889	1	2687	2687	NA	NA
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AA102131 h	H	x	x	210	210	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	211	211	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	212	212	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	213	213	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	214	214	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	215	215	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	216	216	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	217	217	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	218	218	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	219	219	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	220	220	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	221	221	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	222	222	AGC	SGK	2870	889	1	2687	2687	NA	NA
AA102131 h	H	x	x	223	223	AGC	SGK	2870	889	1	2687	2		

Table 1 (cont'd)

Gene Name	SP	Priv Seq ID NA	Priv Seq ID AA	SEQ ID # na	SEQ ID # aa	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeat	CHR localization
BON3 h	1	1	1	84	184	Other	C28C2 ce	2164	535	113	1717	1608	248-267	NA
AA711629 m	148	164	164	65	185	Other	C28C2 ce	1568	378	1	1134	1134	1	NA
AA089102 h CalMKKB	132	186	186	68	185	Other	CAMKK	1767	368	1	1764	1764	65-84	12q23-q14
5F669 17 2 h	158	170	170	67	187	Other	CTRI	3387	241	1850	2572	723	499-521	NA
H5811 h	134	170	170	68	189	Other	DYRK	3893	1171	183	3695	3513	1326-1348	CHR7
AA02163 h DYRK3	133	169	169	69	189	Other	DYRK	2141	553	253	1911	1659	1	NA
AA589241 m DYRK3	133	169	169	70	190	Other	DYRK	2141	553	253	1911	1659	1	NA
5F72 16 2 h R19927 h	109	112	112	71	191	Other	EPR	5163	1649	20	4866	4947	1	NA
R43324 h R19927 h	111	114	114	73	192	Other	EPR	5163	1649	20	4866	4947	1	NA
17000057519457 h	111	114	114	74	193	Other	Endop	3055	253	219	977	759	2283-2365	NA
AA013524 m	135	171	171	75	194	Other	Endop	926	218	1	848	848	1	NA
17000139801197 h IRAK1	137	173	173	76	195	Other	IRAK	1791	590	1	1788	1788	1	NA
AA840598 m IRAK1	137	173	173	77	199	Other	IRAK	2243	362	1	1175	1176	1	NA
AA08547 h	138	174	174	78	197	Other	IRE	2769	922	1	2168	2168	1	NA
HGP 6544466	139	175	175	79	198	Other	KYK2 dd	1857	322	179	1144	986	1	NA
AA449547 m	115	116	116	80	199	Other	KYK2 dd	1251	280	2	841	840	602-621	NA
5F57 10 2 m TESK2 m	115	116	116	81	200	Other	KYK2 dd	140	41	2	124	123	1	NA
AA232253 h	117	118	118	82	201	Other	MLK	2403	800	1	2400	2400	1	NA
A1375137 h	209	210	210	83	202	Other	MLK	2509	835	1	2505	2505	2219-2238	NA
H97685 h	143	178	178	84	203	Other	RIP	2364	634	161	2092	1802	1	10q31
W20810 m	144	180	180	85	204	Other	RIP	1073	289	3	689	687	1	NA
AA744236 h	211	212	212	86	205	Other	SCY1 sc	2067	688	1	2064	2064	1	1q23
A052250 h	225	228	228	87	208	Other	SCY1 sc	1739	505	174	1699	1515	1	NA
AA278642 h	164	200	200	88	207	Other	SCY1 sc	2668	808	105	2528	2424	1764-1783	11q12-q13 Amplicon
AA599286 h	145	181	181	89	208	Other	SLOB7	1949	640	1	1949	1949	1	NA
AA457225 h	146	182	182	90	209	Other	SRPK	1802	533	1	1599	1599	1	NA
SGK022 h	1	1	1	91	210	Other	STK22A	1038	268	184	887	804	1	NA
AA080026 m SGK022 m	149	185	185	92	211	Other	STK22A	1004	268	147	950	804	1	NA
AA39869 h	150	186	186	93	212	Other	STK22A	1537	262	372	1244	876	1	14p11-q11
AA756539 h	151	187	187	94	213	Other	STK22A	1322	358	101	1174	1074	1	NA
AA483975 h	153	189	189	95	214	Other	TSK	822	273	1	819	819	1	NA
AA905446 h	223	224	224	96	215	Other	TSK	1069	216	365	1012	849	1	NA
H29974 h	66	102	102	97	216	Other	UNC	1635	333	2	1000	989	1	NA
AA48804 m H29974 m	155	191	191	98	217	Other	UNC	1490	412	1	1238	1238	701-729	NA
AA215311 h	155	191	191	99	218	Other	UNC	2011	341	189	1221	1023	1	NA
AA018191 h	154	190	190	100	219	Other	UNC	2759	481	113	1555	1443	1	15q23
AA311714 h	155	192	192	101	220	Other	UNC	1876	565	135	1833	1695	1	NA
SGK384 h	108	108	108	102	221	Other	Uncue	117	39	1	117	117	1	NA
AA210451 m SGK384 m	108	108	108	103	222	Other	Uncue	2121	349	222	1268	1047	225-2286	NA
SGK071 2 h	104	104	104	104	223	Other	Uncue	2115	704	1	2112	2112	57-76, 218-337	NA
AA118352 m SGK071 m	161	197	197	105	224	Other	Uncue	1729	840	3	1622	1620	1	NA
1885339 h	162	199	199	106	225	Other	Uncue	2461	540	1	1620	1620	240-259	NA
AA396801 m	163	199	199	107	226	Other	Uncue	1868	365	3	1097	1095	1	NA
AA871275 h VRK3	163	199	199	108	227	Other	VRK	1425	474	1	1422	1422	1	18q13
ST1575 m VRK3 m	163	199	199	109	228	Other	VRK	1009	234	3	704	702	937-957	NA
AA432647 h MPSK1	138	172	172	110	229	Other	VPL238 sc	918	305	1	815	815	1	3cen-3021
H05721 h	168	202	202	111	230	Other	Y098 ce	2668	581	95	1637	1743	1	1022-331 Amplicon
A08585 h	86	100	100	112	231	STE	NEK	2463	699	7	2100	2094	1	NA
AA838348 h	120	124	124	113	232	STE	NEK	2511	839	1	2508	2508	1	NA
R66668 h MKK6	121	125	125	114	233	STE	STE11	3036	1011	1	3033	3033	1	1p32.3-p31.1
PAK6 h 5895-20-11	219	220	220	115	234	STE	STE20-02	2160	719	1	2157	2157	1	20q12
SGR1K106 h 2841-9-4 h	128,127	130,130	130,130	116	235	TK	RTK-20	2460	495	1	1485	1485	1	12p12.3
AA086024 m	128,127	130,130	130,130	117	236	TK	RTK-20	1793	163	1	549	549	1	NA
SGK2alpha h	87	101	101	118	237	AGC	SGK	1812	387	88	1168	1101	1	NA
H08950 h CORK	87	101	101	120	238	CAGC	COK	1359	452	1	1356	1356	1	9q21.1-q21.3
NM 007170 h TESK2	1	1	1	121	239	Other	LINK	3016	555	398	2090	1665	1	NA

Table 2

SP ID# na	Patent Seq	Family	Group	ncraa	Length	ID match	% identity	% Similar	Match	Description	Kinase Domain(s) start	Kinase Domain(s) end	Profile start	Profile end
H 1	122	AGC	GRK	2.7e-314	688	887	100	100	ACC#	BAR22 [Homo sapiens]	191	453	1	261
M 2	123	AGC	GRK	1.30E-190	378	371	98	89	NP 037029.1	Adreneglor receptor kinase, beta 2 (G-protein-linked receptor kin)	3	143	121	261
H 3	124	AGC	GRK	1.30E-190	419	282	71	86	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	26	286	1	261
H 4	125	AGC	GRK	1.30E-190	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	261
H 5	126	AGC	GRK	1.30E-190	729	729	100	100	NP 037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
H 6	127	AGC	GRK	1.30E-190	329	73	46	66	BAA76817.1	KIAA0973 protein [Homo sapiens]	35	310	1	261
M 7	128	AGC	GRK	1.30E-190	88	42	49	71	AAF55594.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	261
H 8	129	AGC	GRK	1.30E-190	484	463	100	100	BAA76809.1	KIAA0963 protein [Homo sapiens]	90	363	1	261
H 9	130	AGC	GRK	1.30E-190	978	615	67	80	NP 002733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H 10	131	AGC	GRK	1.30E-190	105	42	42	57	P05127	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H 11	132	AGC	GRK	1.30E-190	890	890	100	100	NP 05804.1	Protein kinase C, nu [Homo sapiens]	576	832	1	261
H 12	133	AGC	GRK	1.30E-190	889	889	100	100	NP 037487.1	PKNbeta [Homo sapiens]	559	818	1	261
M 13	134	AGC	GRK	1.30E-190	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	125	261
H 14	135	AGC	GRK	1.30E-190	384	94	38	55	AAC62495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	261
H 15	136	AGC	GRK	1.30E-190	469	499	100	100	NP 036556.1	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapiens]	225	459	1	261
H 16	137	AGC	GRK	1.30E-190	745	745	100	100	NP 055311.1	Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapiens]	73 & 428	330 & 683	1	261
H 17	138	AGC	GRK	1.30E-190	549	549	100	100	AAC30182.1	Unknown [Homo sapiens]	153	539	1	261
H 18	139	AGC	GRK	1.30E-190	431	430	100	100	AAD41091.1	SGK [Homo sapiens]	98	355	1	261
M 19	140	AGC	GRK	1.30E-190	426	426	100	100	NP 035491.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	261
M 20	141	AGC	GRK	1.30E-190	244	244	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	169	24	261
H 21	142	AGC	GRK	1.30E-190	349	349	100	100	NP 009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	162	389	1	261
H 22	143	AGC	GRK	1.30E-190	440	440	100	100	CAA04119.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	40	333	1	261
H 23	144	AGC	GRK	1.30E-190	699	466	65	77	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Mus musculus]	368	625	1	261
M 24	145	AGC	GRK	1.30E-190	297	199	67	83	AAF26675.1	CPG16 [Mus musculus]	59	297	1	261
M 25	146	AGC	GRK	1.30E-190	708	181	44	60	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Mus musculus]	415	673	1	261
M 26	147	AGC	GRK	1.30E-190	806	147	55	73	AAF76675.1	CPG16 [Mus musculus]	514	771	1	261
M 27	148	AGC	GRK	1.30E-190	372	372	100	100	NP 004217.1	Death-associated protein kinase-related 2	33	293	1	261
H 28	149	AGC	GRK	1.30E-190	372	340	91	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	261
M 30	150	AGC	GRK	1.30E-190	414	414	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	261
H 31	151	AGC	GRK	1.30E-190	1311	1053	80	80	BAA76843.1	Hypothetical protein F49C5.4 - (Caenorhabditis elegans)	8	259	1	261
H 32	152	AGC	GRK	1.30E-190	436	153	51	70	T22427	Hypothetical protein F49C5.4 - (Caenorhabditis elegans)	74	325	1	261
H 33	153	AGC	GRK	1.30E-190	436	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
H 34	154	AGC	GRK	1.30E-190	729	729	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	59	340	1	261
M 35	155	AGC	GRK	1.30E-190	462	462	100	100	AAC33487.1	R31237.1, partial CDS [Homo sapiens]	999	1258	1	261
M 36	156	AGC	GRK	1.30E-190	1330	1235	100	100	BAA09484.1	KIAA0135 gene, related to p1m-1 oncogene, [Homo sapiens]	1	156	23	261
M 37	157	AGC	GRK	1.30E-190	230	183	79	85	BAA09484.1	KIAA0135 gene, related to p1m-1 oncogene, [Homo sapiens]	20	271	1	261
H 38	158	AGC	GRK	1.30E-190	926	636	100	100	BAA34501.1	KIAA0781 protein [Homo sapiens]	20	271	1	261
H 39	159	AGC	GRK	1.30E-190	629	367	57	69	NP 056655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	261
H 40	160	AGC	GRK	1.30E-190	714	714	100	100	NP 054401.1	Homomally upregulated neu tumor-associated kinase [Homo sapiens]	61	320	1	261
H 41	161	AGC	GRK	1.30E-190	874	211	63	80	AAAT73168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	570	825	1	261
H 42	162	AGC	GRK	1.30E-190	2268	2227	100	100	BAA92535.1	KIAA1297 protein [Homo sapiens]	620 & 1086	873 & 1356	1	261
H 43	163	AGC	GRK	1.30E-190	127	67	99	99	BAA92535.1	KIAA1297 protein [Homo sapiens]	3	78	186	261
H 44	164	AGC	GRK	1.30E-190	1287	1284	100	100	NP 006995.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	985	1239	1	261
H 45	165	AGC	GRK	1.30E-190	514	114	41	63	P25323	MLCK [Dictyostelium discoideum]	116	381	1	261
H 46	166	AGC	GRK	1.30E-190	508	181	53	65	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H 47	167	AGC	GRK	1.30E-190	478	188	57	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	261
H 48	168	AGC	GRK	1.30E-190	268	139	62	79	NP 038527.1	PFTARE protein kinase, 1 [Homo sapiens]	1	216	23	261
H 49	169	AGC	GRK	1.30E-190	247	146	59	75	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	191	23	261

Table 2 (cont'd)

M 50	170	CMGC	CDK	2.90E-64	296	193	65	78	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H 51	171	CMGC	CDK	1.10E-264	1490	1490	100	100	AAF38401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H 52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF38509.1	NKIAMRE [Homo sapiens]	4	385	1	261
M 53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M 54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP_036251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
H 55	175	CMGC	CLK	1.50E-242	499	436	91	93	NP_031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H 56	176	CMGC	RCK	9.10E-89	544	343	57	64	AAD12179.1	Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus]	13	305	1	261
H 57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP_055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H 58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M 59	179	CMGC	RCK	1.60E-79	413	198	60	77	P20669	MLCK [Rattus norvegicus]	109	364	1	261
H 60	180	Microbial PK	GR262 sc	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
H 61	181	Other	C26C2 ce	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	267	1	261
M 62	182	Other	C26C2 ce	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
M 63	183	Other	C26C2 ce	6.70E-300	1952	1193	99	99	NP_055638.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H 64	184	Other	C26C2 ce	1.10E-254	535	535	100	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M 65	185	Other	C26C2 ce	2.50E-208	378	372	98	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H 66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31507.1	Caz+/calmodulin-dependent protein kinase beta [Homo sapiens]	165	446	1	261
H 67	187	Other	CTR1	9.90E-24	287	87	33	52	QJ1743	Hypothetical 33.6K protein - rabbit fibroma virus	24	285	1	261
H 68	188	Other	DYRK	0	1171	1137	97	99	AAD52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H 69	189	Other	DYRK	2.10E-280	553	553	100	100	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M 70	190	Other	DYRK	2.30E-95	168	149	90	96	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H 71	191	Other	EIFK	0	1649	1493	90	96	NP_038747.1	GCN2 eIF2alpha kinase [Mus musculus]	167	583	1	261
H 73	192	Other	EIFK	1.50E-220	630	630	100	100	NP_055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	101	187	65	147
H 74	193	Other	Endop	2.50E-45	253	102	45	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	116	150	116	147
M 75	194	Other	Endop	3.70E-45	216	100	45	64	AAF50799.1	(AE003587) CG10673 gene product [Drosophila melanogaster]	165	443	1	261
M 76	195	Other	IRAK	0	596	596	100	100	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
M 77	196	Other	IRAK	1.20E-170	392	293	75	85	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	516	777	1	261
H 78	197	Other	IRE	1.5e-323	922	746	82	89	NP_036146.1	Ire1, inositol-requiring 1 gene [Mus musculus]	32	318	1	261
H 79	198	Other	KYK2 dd	8.70E-40	225	102	45	82	AAF48758.1	CG1173 gene product [Drosophila melanogaster]	12	266	1	261
M 80	199	Other	KYK2 dd	5.90E-32	280	109	32	50	AAF48758.1	CG1173 gene product [Drosophila melanogaster]	12	266	1	261
M 81	200	Other	LMK	2.60E-17	41	37	92	95	NP_009101.1	lesls-specific kinase 2 [Homo sapiens]	18	259	1	261
H 82	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	483	723	1	261
H 83	202	Other	MLK	8.60E-251	835	835	100	100	AAD29632.1	Putative protein-tyrosine kinase [Homo sapiens]	357	620	1	261
H 84	203	Other	RIP	2.20E-158	634	365	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	7	27	181	202
M 85	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	57	83	50	78
H 86	205	Other	SCY1 sc	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	32	327	1	261
H 87	206	Other	SCY1 sc	1.70E-209	505	354	98	98	BAA92598.1	KIAA1360 protein [Homo sapiens]	65	131	47	116
H 88	207	Other	SCY1 sc	2.20E-157	808	396	45	61	AAF56933.1	CG1973 gene product [Drosophila melanogaster]	230	305	81	143
H 89	208	Other	SLOB?	7.40E-196	649	649	100	100	BAA91097.1	Unamed protein product [Homo sapiens]	79	531	1	261
H 90	209	Other	SRPK	5.80E-252	533	533	100	100	NP_055185.1	Serine/threonine kinase 23 [Homo sapiens]	10	265	1	261
H 91	210	Other	STK22A	3.80E-53	268	122	46	70	NP_033461.1	Serine/threonine kinase 22A (Spermogenesis associated) [Mus musculus]	25	280	1	261
M 92	211	Other	STK22	2.70E-52	268	127	48	68	NP_033461.1	Serine/threonine kinase 22B (Spermogenesis associated) [Mus musculus]	12	272	1	261
H 93	212	Other	STK22A	4.60E-16	292	112	45	64	NP_033461.1	Serine/threonine kinase 22A (Spermogenesis associated) [Mus musculus]	12	267	1	261
H 94	213	Other	TSK	5.10E-123	358	322	90	96	NP_033462.1	Serine/threonine kinase 22B (Spermogenesis associated) [Mus musculus]	1	213	7	261
H 95	214	Other	TSK	2.10E-33	273	122	46	62	NP_033462.1	Serine/threonine kinase 22B (Spermogenesis associated) [Mus musculus]	1	329	1	261
H 96	215	Other	TSK	2.50E-32	216	93	41	58	NP_033462.1	Serine/threonine kinase 22B (Spermogenesis associated) [Mus musculus]	80	408	1	261
H 97	216	Other	UNC	0.000062	333	57	36	56	AAD32787.1	Putative protein kinase [Arabidopsis thaliana]	8	340	1	261
M 98	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase [ULK] 2 [Mus musculus]	57	313	1	261
H 99	218	Other	UNC	0.001096	341	50	36	56	BAA77341.1	UNC-51-like kinase [ULK] 2 [Mus musculus]	4	285	1	261
H 100	219	Other	UNC	1.90E-68	480	247	100	100	T17265	Hypothetical protein DKFZp434C131.1 - human (fragment)	4	285	1	261
H 101	220	Other	UNC	1.60E-208	565	468	96	96	BAA91270.1	Unamed protein product [Homo sapiens]	1	39	84	124
H 102	221	Other	Unique	6.70E-10	39	27	69	90	AAD00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M 103	222	Other	Unique	0.00022	349	38	30	50	CAA18116.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H 104	223	Other	Unique	0.000128	704	54	30	45	BAA88578.1	KIAA1284 protein [Homo sapiens]	1	246	25	261
M 105	224	Other	Unique	0.007385	540	25	42	61	AAF47916.1	Tie gene product [Drosophila melanogaster]	9	104	188	261
H 106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M 107	226	Other	Unique	0.022948	365	25	34	57	NP_006276.1	Testis-specific kinase 1 [Homo sapiens]	68	96	42	71
H 108	227	Other	VRK	3.10E-263	474	474	100	100	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M 109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H 110	229	Other	YPL236.sc	7.40E-144	305	304	100	100	AAC28337.1	MPSK [Homo sapiens]	20	290	1	261
H 111	230	Other	YQ09.ce	5.10E-49	581	135	43	63	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H 112	231	STE	NEK	3.30E-30	698	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H 113	232	STE	NEK	2.70E-119	836	357	86	86	AAD31938.1	[AC007055] unknown [Homo sapiens]	52	308	1	261
H 114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004863.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	376	629	6	261
H 115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H 116	235	TK	RTK-20	4.90E-24	495	77	38	56	AA088465.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	261
M 117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H 118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H 120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	267	1	261
H 121	239	Other	LIMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

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Table 3

Tissue	Tumor - sym	Normal - sym	Tumor - to	Tumor cells	Normal	Endos	p33	SEQ 003	AKED 1	TBX	SEQ 006	AKED 2	AKED 3	CAESD 1	EP	SEQ 12	PH	SEQ 14	HK	SEQ 16	RS
adrenal gland - h	7	13811	543727	29445	341051	56584	11605	7420	13811	543727	29445	341051	56584	11605	7420	13811	543727	29445	341051	56584	11605
lymph node - h	7	8151	32265	1202494	118257	105718	55339	19991	8151	32265	1202494	118257	105718	55339	19991	8151	32265	1202494	118257	105718	55339
bone marrow - h	3	4465	9236	1477566	35367	32271	33650	13151	4465	9236	1477566	35367	32271	33650	13151	4465	9236	1477566	35367	32271	33650
mammary gland - h	4	964	316	1098677	4031	4318	1084	1993	964	316	1098677	4031	4318	1084	1993	964	316	1098677	4031	4318	1084
breast - h	5	968	5273	229783	54222	21862	7501	774	968	5273	229783	54222	21862	7501	774	968	5273	229783	54222	21862	7501
pancreas - h	6	5433	3574	334665	50925	32290	8511	11829	5433	3574	334665	50925	32290	8511	11829	5433	3574	334665	50925	32290	8511
carotid - h	7	6350	19704	767223	84606	35457	16370	29263	6350	19704	767223	84606	35457	16370	29263	6350	19704	767223	84606	35457	16370
pituitary gland - h	8	8542	7686	712184	80497	38563	19473	11010	8542	7686	712184	80497	38563	19473	11010	8542	7686	712184	80497	38563	19473
testis - h	9	13719	6945	961041	85491	30156	23431	13781	13719	6945	961041	85491	30156	23431	13781	13719	6945	961041	85491	30156	23431
placenta - h	10	5763	15456	1232178	46205	45070	24271	13087	5763	15456	1232178	46205	45070	24271	13087	5763	15456	1232178	46205	45070	24271
testis - h	11	4707	10839	537527	51063	67946	31171	19988	4707	10839	537527	51063	67946	31171	19988	4707	10839	537527	51063	67946	31171
prostate - h	12	3477	1784	122058	60267	49912	11799	9464	3477	1784	122058	60267	49912	11799	9464	3477	1784	122058	60267	49912	11799
testis - h	13	3302	5294	1248111	26196	35129	17029	10418	3302	5294	1248111	26196	35129	17029	10418	3302	5294	1248111	26196	35129	17029
salivary gland - h	14	2725	3698	428781	37947	37758	11433	13005	2725	3698	428781	37947	37758	11433	13005	2725	3698	428781	37947	37758	11433
testis - h	15	6315	6461	1305487	79678	56484	31011	34594	6315	6461	1305487	79678	56484	31011	34594	6315	6461	1305487	79678	56484	31011
skelatal muscle - h	16	5483	2765	187692	81052	12319	10683	11874	5483	2765	187692	81052	12319	10683	11874	5483	2765	187692	81052	12319	10683
heart - h	17	3012	1915	227404	27479	26473	6357	11717	3012	1915	227404	27479	26473	6357	11717	3012	1915	227404	27479	26473	6357
small intestine - h	18	3020	5561	335116	28567	28583	11720	12229	3020	5561	335116	28567	28583	11720	12229	3020	5561	335116	28567	28583	11720
kidney - h	19	358	5453	413001	41491	24102	7820	8496	358	5453	413001	41491	24102	7820	8496	358	5453	413001	41491	24102	7820
spinal cord - h	20	5186	2799	224006	21586	12872	12294	4444	5186	2799	224006	21586	12872	12294	4444	5186	2799	224006	21586	12872	12294
testis - h	21	3163	4478	238587	24563	16261	11556	8365	3163	4478	238587	24563	16261	11556	8365	3163	4478	238587	24563	16261	11556
Spleen - h	22	3364	1518	206605	46111	29975	10799	8189	3364	1518	206605	46111	29975	10799	8189	3364	1518	206605	46111	29975	10799
lung - h	23	4121	1921	488627	25513	25347	10630	4418	37827	7084	4121	1921	488627	25513	25347	10630	4418	37827	7084	4121	1921
stomach - h	24	2820	419	312852	33861	12206	5870	3999	12801	5109	2820	419	312852	33861	12206	5870	3999	12801	5109	2820	419
testis - h	25	6342	15392	1250953	99041	19148	117943	9666	44950	11194	6342	15392	1250953	99041	19148	117943	9666	44950	11194	6342	15392
thyroid - h	26	7656	4995	1874062	129088	83645	46501	31139	8525	13765	7656	4995	1874062	129088	83645	46501	31139	8525	13765	7656	4995
HPAEC	28	7304	0	86668	34171	26774	3919	14479	67087	8110	7304	0	86668	34171	26774	3919	14479	67087	8110	7304	0
thyroid gland - h	29	3870	1073	194311	42836	25961	9827	9143	43670	6892	3870	1073	194311	42836	25961	9827	9143	43670	6892	3870	1073
RPTEC	30	24571	10273	80360	21213	3351	3397	15054	42740	7144	24571	10273	80360	21213	3351	3397	15054	42740	7144	24571	10273
stomach - h	31	6724	3097	60783	60945	49813	15260	10042	76255	11073	6724	3097	60783	60945	49813	15260	10042	76255	11073	6724	3097
HMEC	32	7791	1355	139606	24427	15301	4715	17173	65164	3038	7791	1355	139606	24427	15301	4715	17173	65164	3038	7791	1355
uterus - h	33	5386	4649	634257	34433	33971	14725	15085	66678	8640	5386	4649	634257	34433	33971	14725	15085	66678	8640	5386	4649
HCAEC	34	7676	0	52247	26246	12123	1758	28455	51717	8203	7676	0	52247	26246	12123	1758	28455	51717	8203	7676	0
pancreas - h	35	11088	5105	15818	14140	15818	8345	46413	46413	11345	11088	5105	15818	14140	15818	8345	46413	46413	11345	11088	5105
lymph node - h	36	6132	731	47839	15791	20735	8420	3812	64078	1285	6132	731	47839	15791	20735	8420	3812	64078	1285	6132	731
Skeletal muscle - h	37	5906	77	0	11060	5411	5264	2070	30349	3453	5906	77	0	11060	5411	5264	2070	30349	3453	5906	77
testis - h	38	6880	2171	144493	18355	15506	5456	2447	56121	9104	6880	2171	144493	18355	15506	5456	2447	56121	9104	6880	2171
heart - h	39	7091	745	15301	9551	25115	3925	3048	61910	10342	7091	745	15301	9551	25115	3925	3048	61910	10342	7091	745
thyroid - h	40	9710	2477	87220	40613	17473	10164	70722	10210	11345	9710	2477	87220	40613	17473	10164	70722	10210	11345	9710	2477
Ductum - h	41	2879	0	28026	9776	14899	4049	9070	42191	6586	2879	0	28026	9776	14899	4049	9070	42191	6586	2879	0
testis - h	42	12395	3365	21478	20505	16311	15818	3363	56960	9323	12395	3365	21478	20505	16311	15818	3363	56960	9323	12395	3365
Salivary gland - h	43	4496	1134	12171	4150	12171	4150	2393	25172	8767	4496	1134	12171	4150	12171	4150	2393	25172	8767	4496	1134
uterus - h	44	6962	23669	33514	19562	14956	17932	4385	51204	8767	6962	23669	33514	19562	14956	17932	4385	51204	8767	6962	23669
HT218-normal		115	357	6191	3368	2191	1738	134	12858	1034	115	357	6191	3368	2191	1738	134	12858	1034	115	357
HT213-normal		363	0	427	9712	1918	0	144	10801	8245	363	0	427	9712	1918	0	144	10801	8245	363	0
HT157-normal		362	0	12	25470	123	1230	654	16328	11860	362	0	12	25470	123	1230	654	16328	11860	362	0
Bov-13		356	356	6533	1666	563114	49109	10630	20146	87144	356	356	6533	1666	563114	49109	10630	20146	87144	356	356
Bov-12		354	354	11250	1285	58750	69954	9439	12012	3467	354	354	11250	1285	58750	69954	9439	12012	3467	354	354
carotid - h		344	0	242	21691	2939	1748	3951	12437	27729	344	0	242	21691	2939	1748	3951	12437	27729	344	0
breast - h		342	0	563	20341	2890	0	2454	2220	31405	342	0	563	20341	2890	0	2454	2220	31405	342	0
RPTEC		334	334	0	29114	24733	2279	333	80511	719031	334	334	0	29114	24733	2279	333	80511	719031	334	334
lymph node - h		332	704	0	1941	7347	7055	14451	1180	30798	332	704	0	1941	7347	7055	14451	1180	30798	332	704
h adult SAMC 10/21/92 #17		330	605	0	6514	6587	1044	0	540	47380	330	605	0	6514	6587	1044	0	540	47380	330	605
testis - h		328	7199	318	131277	49026	10433	8686	29172	70959	328	7199	318	131277	49026	10433	8686	29172	70959	328	7199
HT308-normal		327	0	217335	6222	320	8648	627	50874	7284	327	0	217335	6222	320	8648	627	50874	7284	327	0
thyroid - h		326	6784	80	239220	54119	10534	7917	2366	70826	326	6784	80	239220	54119	10534	7917	2366	70826	326	6784
HT149 - normal		321	187	61	901	2827	0	156	1743	41371	321	187	61	901	2827	0	156	1743	41371	321	187
HEPM M1 unselected		320	320	0	8126	12132	3937	4153	3048	61910	320	320	0	8126	12132	3937	4153	3048</			

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor-to	Tumor cells	Normal	Endo	p53	SEQ 003	AGEO 3	TBR	SEQ 004	AGEO 4	AGEO 5	CAR	SEQ 11	EP	SEQ 17	SEQ 14	SEQ 16	#
He 578T	155							12571	0	186624	345411	16731	127121	50761	460431	5514				
MCF-7/ADR-RES	153							13420	1292	37520	28262	9797	5784	88701	46543	5188				
MCF7	151							15337	1095	930587	52916	21779	15050	10792	53949	9415				
UACC-257	147							5452	566	204412	17174	10734	18318	7544	63303	4435				
UACC-62	145							11456	0	155616	13667	10437	42807	4588	32000	8337				
SK-MEL-28	144							2455	123	56725	21571	11116	27564	1929	27441	4551				
UO-31	143							4479	0	350827	13751	7222	29647	2124	20351	5624				
SK-MEL-5	142							6357	0	217414	15138	8047	23531	1186	46282	5242				
BM-12	141							5444	690	436806	16465	4434	30762	7048	29301	5242				
SK-MEL-2	140							5033	377	43470	12308	4099	4523	7794	30992	3137				
HCT-15	139							2946	331	351803	16006	13917	13874	7005	30577	5799				
MDAMB-36	138							1187	0	352955	14372	9250	17403	5476	54739	10743				
COLO 205	137							6590	0	403468	18570	6670	21327	8334	45060	7827				
LOX IMVI	136							5349	0	384005	16795	8554	17491	4868	57736	10848				
SW-620	135							4200	204	1678684	23713	10725	23514	5599	20010	7615				
TIC-8	134							11820	0	622556	16554	5952	105144	2213	38849	5702				
HCT 116	133							3536	1562	130533	21155	7332	9162	42011	43207	6844				
T86-0	132							3482	0	184816	13660	7383	8546	4065	37409	5317				
MCC-2998	131							3264	0	206284	17720	4992	13644	5047	34175	6677				
ACHN	130							6370	2297	398066	17568	5781	10039	3671	62363	8455				
PC-3	129							8682	177	84811	18456	10350	9438	4663	36060	5785				
RUF 383	128							12090	0	48624	14186	4679	6473	3508	35272	6853				
DU-145	127							5033	279	469833	21616	7110	11090	3324	40444	5886				
C6-36	126							10928	136	30508	12131	3150	3940	2461	37777	3203				
SR	125							3045	722	712846	12748	8899	13451	4297	35215	6467				
A498	124							3565	257	420391	13247	3620	10151	2543	37659	4327				
RPMI 8226	123							9123	0	84349	18090	41974	17229	4374	39104	6293				
UW-2C	122							2279	0	272834	18299	3418	26799	1191	54853	6646				
H-60	121							6263	217	202877	17152	14156	20787	3796	32518	5287				
MOLT-4	120							1142	0	137022	6968	5329	22423	4164	36440	4569				
OVCA8-5	119							4384	0	440040	12768	10231	15496	2066	28309	4478				
H-562	118							2620	368	1086525	16534	5732	11960	4117	25375	6624				
OVCA4-1	117							2150	190	804713	14187	8845	24923	5410	54115	2984				
CCRF-CEM	116							2856	3587	4965335	16528	8040	17237	5681	47598	8203				
U4-539	115							4910	0	3589707	21767	9518	81643	9569	36120	4574				
HOP-62	114							1311	0	551868	10974	7064	21926	5119	52017	5813				
SF-295	113							4819	0	1887878	13841	4718	16931	7024	34603	6113				
ASJWATCC	112							2174	369	345760	13736	5656	11035	3280	19576	4413				
SF-708	111							11905	716	68183	16107	8440	7164	2565	40830	7967				
NCH-HS2	110							17217	599	378650	27722	12358	16617	5368	47439	8326				
LZ751	109							3054	1351	233341	16600	6551	11824	2278	35243	5718				
NCH-HS2	108							4147	0	1126364	19715	10185	32962	3153	44511	8645				
NCH-HS2	107							8539	373	230300	18796	8509	12059	5746	540761	8260				
NCH-HS2	106							6777	0	452533	13060	6899	18903	4436	24896	5244				
NCH-HS2	105							2579	630	27182	8638	7216	8638	2872	41106	4518				
NCH-HS2	104							6471	921	580327	19449	14478	10523	3322	49937	6532				
NCH-HS2	103							7350	0	219881	17548	7956	12434	3102	50554	5744				
SK-OV-3	102							32959	310	108348	20896	10725	24197	3054	61587	8993				
NCH-HS2	101							9451	0	822763	15647	7476	11071	1291	33110	2984				
IGROV1	100							5614	371	109502	13285	6342	15724	2809	30481	3518				
ERKX	99							18002	768	313545	14157	9518	9579	2981	41869	3318				
OVCA8-8	98							6208	1110	359816	18612	6437	21788	2010	25017	2624				
HOP-62	97							17781	814	16774	10361	4170	6094	3129	31126	4098				
H-60	96							7808	0	317849	22815	4246	39600	3282	33300	3960				
H-60	95							11095	0	177631	18163	6067	4047	3578	30990	4127				
H-60	94							4478	137	80771	14410	12690	2296	588	30937	5335				
H-60	93							13602	340	155425	23184	8658	14419	3871	20126	5742				
TCGP	92							6008	0	558454	15245	18266	10157	3439	22853	6471				
AS49-1	91							1491	8421	44905	11718	0	0	0	0	0				
AS49-3	90							139	4212	26336	6707	0	0	0	0	0				
AS49-4	89							278	5323	38473	10536	0	0	0	0	0				
AS49-5	88							480	2872	28588	10727	0	0	0	0	0				
AS49-7	87							148	162	15733	8786	0	0	0	0	0				
ERKX-1	86							848	143	89074	18784	0	0	0	0	0				
ERKX-2	85							1400	43690	78323	25010	0	0	0	0	0				
ERKX-3	84							935	834	22807	12511	0	0	0	0	0				
ERKX-5	83							0	0	58003	7740	0	0	0	0	0				
ERKX-7	82							725	1578	28692	11042	0	0	0	0	0				
MCF-7-1	81							840	718	50119	10699	0	0	0	0	0				
MCF-7-3	80							607	6245	68350	7863	0	0	0	0	0				
MCF-7-4	79							839	1155	140711	14817	0	0	0	0	0				
MCF-7-5	78							224	1050	81146	11010	0	0	0	0	0				
MCF-7-7	77							0	1331	10567	6726	0	0	0	0	0				
ADR-RES-1	76							0	3085	51125	18485	0	0	0	0	0				
ADR-RES-3	75							425	525	27534	8062	0	0	0	0	0				
ADR-RES-4	74							0	15470	44449	0	0	0	0	0	0				
ADR-RES-5	73							268	473	35606	7549	0	0	0	0	0				
ADR-RES-7	72							0	7502	12923	13062	0	0	0	0	0				
WI 38-1	71							619	0	41827	24067	0	0	0	0	0				
WI 38-3	70							508	217	40670	18323	0	0	0	0	0				
WI 38-4	69							847	751	32710	9317	0	0	0	0	0				
WI 38-5	68							1151	3721	17091	11387	0	0	0	0	0				
WI 38-7	67							218	4617	64191	12288	0	0	0	0	0				
HPV E6	66							532	12621	65453	13319	0	0	0	0	0				
HPV E6	65							460	6431	51037	17033	0	0	0	0	0				
HPV E6	64							802	33111	48269	7885	0	0	0						

Tissue	Tumor type	Normal type	Tumor - to	Tumor cells	Normal	Endos	p33	SEQ 001	A5EO 3	TBM50	894	A9EO 000	A9EO 8	CAR	SEQ 11	EP5EO 12	PK5EO 14	HP5EO 16	RS
DuPang-7								4091	4153	130751	48007	0	0	0	0	0	0	0	0
DuPang-8								1843	0	129784	31568	0	0	0	0	0	0	0	0
DuPang-9								1704	352	23137	22363	0	0	0	0	0	0	0	0
DuPang-11								2364	2910	56036	34353	0	0	0	0	0	0	0	0
DuPang-13								1621	0	143418	17464	0	0	0	0	0	0	0	0
DuPang-10								1137	11437	58719	25013	0	0	0	0	0	0	0	0
DuPang-1								1609	0	176675	67121	0	0	0	0	0	0	0	0
DuPang-2								778	282	80117	44173	0	0	0	0	0	0	0	0
DuPang-3								1038	5999	88419	23252	0	0	0	0	0	0	0	0
DuPang-4								44	3575	46050	15499	0	0	0	0	0	0	0	0
DuPang-5								447	217	37705	8958	0	0	0	0	0	0	0	0
DuPang-6								1754	0	104257	34986	0	0	0	0	0	0	0	0
LS40 - 2								141	1853	30654	11740	0	0	0	0	0	0	0	0
EKVX - 8								mutant	201	6488	74732	34175	0	0	0	0	0	0	0
HCT-116 - 7								wt	459	0	45374	15406	0	0	0	0	0	0	0
HCT-116 - 8								wt	360	866	88940	25876	0	0	0	0	0	0	0
HT29 - 1								mutant	293	3501	23154	10610	0	0	0	0	0	0	0
HT29 - 7								mutant	78	3147	6867	6481	0	0	0	0	0	0	0
HT29 - 8								mutant	181	487	50732	18019	0	0	0	0	0	0	0
SF530 - 7								wt	7386	375	15224	6477	0	0	0	0	0	0	0
SF530 - 8								wt	0	0	57678	8738	0	0	0	0	0	0	0
SF-768 - 7								mutant	507	446	33057	13175	0	0	0	0	0	0	0
SF-768 - 8								mutant	807	0	30102	8841	0	0	0	0	0	0	0
OVCAR-4 - 7								wt	891	1395	73107	15862	0	0	0	0	0	0	0
OVCAR-4 - 8								wt	1368	537	105549	21101	0	0	0	0	0	0	0
OVCAR-5 - 7								mutant	0	328	52988	10750	0	0	0	0	0	0	0
OVCAR-5 - 8								mutant	158	0	17818	10967	0	0	0	0	0	0	0
MCF-7 - 8								wt	555	740	24190	11863	0	0	0	0	0	0	0
ADR-RES - 8								wt	822	2013	12544	17722	0	0	0	0	0	0	0
HPV E6								wt	0	2243	23963	6106	0	0	0	0	0	0	0
SW480 - 7								mutant	727	10									

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - to	Tumor - cala	Normal	Endoc	p33	SEQ 17	AA	SEQ 20	SQ	SEQ 32	PT	SEQ 26	AA	SEQ 29	DR	SEQ 31	OR	SEQ 33	AE	40	M45E	844	T
adrenal gland - h	1							46820	1342	187762	8931	11409	24831	66520	5991	4349									
lymph node - h	2							94539	1004	173107	14301	80024	153021	135195	331	2571									
bone marrow - h	3							83024	345	117785	11301	51933	6448	73534	0	794									
pancreas gland - h	4							24735	0	18847	1710	2723	260	5274	154	306									
brain - h	5							54253	1826	188461	6870	925	1184	700301	3190	2311									
pancreas - h	6							71540	2036	48828	7425	7287	2272	31495	4051	1346									
carotid artery - h	8							82436	104	298725	10725	2748	7854	135678	6034	274									
pharynx gland - h	9							87365	232	110587	15543	7314	2404	14670	3055	3472									
total brain - h	10							103271	0	167692	22024	3638	1150	63217	7424	8836									
placenta - h	11							80242	804	105453	8213	8434	6509	126054	1506	4165									
total kidney - h	12							450048	5028	152875	10990	12224	7283	65346	5690	4519									
prostate - h	13							24934	1446	64243	10904	17723	1143	24000	979	86									
total liver - h	14							58677	3153	86695	11342	15732	2410	33364	279	2130									
salivary gland - h	15							60763	0	122533	3600	18767	1080	12909	0	231									
total lung - h	16							92518	1478	187809	6127	19242	4176	61498	1546	3005									
skeletal muscle - h	17							37531	171	575843	2744	1837	505	48674	1077	2017									
heart - h	18							439811	0	296349	885	4850	2245	31329	11021	2114									
small intestine - h	19							42970	1357	80551	3331	14338	2021	21878	632	1627									
kidney - h	20							48325	6757	77677	1793	3203	1359	36570	2144	1494									
spleen - h	21							54755	1215	53517	21274	5273	1063	21487	717	116									
ovary - h	22							40337	3539	53039	4414	2272	1224	34138	1261	413									
stomach - h	23							44668	0	129409	2530	30444	4982	17845	0	627									
lung - h	24							37621	577	103801	816	25788	5316	33759	0	453									
stomach - h	25							18010	963	37850	1810	8095	1906	11633	6651	331									
heart - h	26							44650	98	56303	30895	13224	4542	332139	18061	1333									
thyroid - h	27							85252	631	422519	10169	30950	8722	120548	1732	317									
HPAEC	28							107087	0	3134	3084	2437	1015	4291	0	155									
thyroid gland - h	29							43620	547	161026	4292	4819	836	37702	0	255									
RTPEC	30							42540	30	3012	5372	4367	356	418	0	81									
trachea - h	31							78666	3031	144782	82321	30464	33211	42097	402	2353									
HMEC	32							85164	650	2147	2421	0	3872	1056	0	0									
ovary - h	33							46648	264	142065	5371	8755	1003	37845	7649	3631									
HCAEC	34							51717	3731	22368	2129	110	560	199	242	0									
pancreas - h	35							46443	0	0	4314	13335	0	2589	0	1082									
lymph node - h	36							84078	0	0	5699	83785	2110	7825	0	0									
skeletal muscle - h	37							20349	418	26339	20	319	2093	817	0	0									
total liver - h	38							56121	649	0	2467	9199	1008	7451	9471	250									
heart - h	39							47672	0	2818	3496	1134	0	4366	492	0									
thyroid - h	40							70722	0	0	3341	57019	1466	2672	2201	0									
Duodenum - h	41							41181	141	13831	4470	5601	2529	1091	3081	0									
total brain - h	42							46360	570	0	6154	4108	205	10811	3641	366									
salivary gland - h	43							35172	48	827	1319	17131	0	12051	0	0									
ovary - h	44							57094	129	294	2069	13574	462	3483	376	0									
ovary - h								12948	0	0	2054	9	0	0	0	0									
MT218-normal								363	6245	771	0	240	222	347	3271	561	0								
MT213-normal								361	16329	0	0	248	163	0	542	0	0								
MT181-normal								356	356	1094	0	27325	6795	2232	5309	1480	12								
Beu-13								354	354	0	0	42865	4027	1119	42	476	0								
Beu-12								344	344	0	0	239	839	501	0	711	0								
carotid artery - h								342	31402	290	0	0	80	781	0	0	0								
RTPEC								334	334	178031	0	8004	9599	61	4791	1121	0								
lymph node - h								332	30788	277	337	2691	52827	2521	761	0	0								
in situ SMC 1021/82 #17								328	47300	231	0	788	41	0	273	54	0								
total brain - h								328	70908	0	8377	20585	10509	83	2749	1217	0								
MT308-normal								327	60974	0	0	399	0	396	202	1110	0								
thyroid - h								326	70426	0	634	42378	28181	721	750	326	115								
MT148-normal								321	41371	416	0	0	43	166	325	0									
HEPM 3d untreated								320	61910	0	10739	6705	2992	225	3650	232	0								
ovary - h								318	86453	444	3041	24906	186533	3035	4242	12917	166								
trachea - h								316	46848	514	28803	129836	7113	2740	8021	460	0								
adrenal gland - h								314	44846	0	1464	15601	64896	5240	1896	0	506								
salivary gland - h								311	61687	0	2684	38262	1045	347	0	0	0								
ovary - h								309	47609	525	0	280	25416	895	178	535	0								
pancreas - h								307	24764	118	0	1582	19211	815	378	800	157								
pharynx gland - h								305	44917	0	0	631	13630	1321	520	126	506								
pancreas - h								303	86451	1168	0	8443	102692	7874	407	372	0								
mammary gland - h								302	72421	667	3702	5722	10239	184	4728	1088	50								
stomach - h								298	63198	444	0	35622	93342	8321	7816	1714	0								
ovary - h								297	63254	21	1047	24117	9023	1462	3474	1159	81								
ovary - h								296	53225	0	138	2172	73566	6138	806	0	0								
spleen - h								294	62962	464	0	27722	35430	3183	1043	1150	155								
spleen - h								292	41621	381	0	41621	140156	2505	866	0	153								
small intestine - h								290	60372	0	19	20791	62231	3667	2424	535	896								
skeletal muscle - h								275	50557	27	0	27722	350	0	0	0	0								
bone marrow - h								272	64753	27	0	2305	5560	59	0	0	355								
adrenal gland - h								275	37169	0	0	1157	0	432	0	0	0								

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Table 3 (cont'd)

Tissue	Tumor + ym	Normal + ym	Tumor - 10	Tumor cells	Normal	Endos	p53	SEQ 17	AA	SEQ 20	SEQ 22	PTK	SEQ 26	AA	SEQ 29	DR	SEQ 31	DR	SEQ 32	AA	SEQ 40	MA	SEQ 44	T
Caco-2				166				25641	11	01	7271		811		41121	01	01	01	01	01	01	01	01	01
T47D				168				43253	1415	1044	2462	2283	8374	105	01	01	01	01	01	01	01	01	01	01
K562				169				52705	01	4627	838	771	1518	1109	01	01	01	01	01	01	01	01	01	01
HL60				171				20545	01	218	900	16	85	01	01	01	01	01	01	01	01	01	01	01
CRL 1441 RNA 8/30				181				11952	01	486	1871	242	339	321	197	01	01	01	01	01	01	01	01	01
781T untreated + DNase				183				21315	01	01	01	01	01	01	01	01	01	01	01	01	01	01	01	01
K562 poly A+				194				21962	194	01	1630	2000	1064	365	01	01	01	01	01	01	01	01	01	01
K562 poly A+				195				30104	01	1150	3112	1663	145	01	01	01	01	01	01	01	01	01	01	01
ACHN				198				23610	01	1874	1898	523	874	750	371	126	01	01	01	01	01	01	01	01
UACC-62				200				18193	130	89	1284	812	848	01	550	01	01	01	01	01	01	01	01	01
MCF-7/ADR-RES				202				12681	314	01	714	405	215	178	01	435	01	01	01	01	01	01	01	01
UTOS (Mammary) poly A+				204				8405	01	200	1294	573	149	01	01	01	01	01	01	01	01	01	01	01
WISH (Colo) poly A+				206				12990	01	01	14	01	82	01	309	01	01	01	01	01	01	01	01	01
458 melanoma mRNA				208				83548	01	1041	3506	14092	411	01	411	01	01	01	01	01	01	01	01	01
CCL137 RNA 3/21/85				218				21190	01	563	01	631	47	01	496	01	01	01	01	01	01	01	01	01
W158 72h 0.5% FBS, 2h 10% FBS				219				28050	01	01	3727	01	149	176	134	01	01	01	01	01	01	01	01	01
CRL 1441 + TPA (24h) 8/20				220				14725	01	133	01	01	355	862	01	01	01	01	01	01	01	01	01	01
Kan-1				221				28116	84	8	1488	338	447	157	361	01	01	01	01	01	01	01	01	01
Kan-2				223				32848	50	01	353	01	235	01	01	01	01	01	01	01	01	01	01	01
Kan-4				225				37538	43	84	154	01	22	01	887	01	01	01	01	01	01	01	01	01
HOP-82				241				22249	01	01	58	726	740	63	01	01	01	01	01	01	01	01	01	01
MOL T-4				242				18708	01	1383	142	22	3064	636	01	50	01	01	01	01	01	01	01	01
FKVX				243				22457	387	303	1836	537	2757	371	01	01	01	01	01	01	01	01	01	01
HL 60				244				33145	01	01	01	01	4255	2903	01	01	01	01	01	01	01	01	01	01
HEL427				245				29842	890	901	308	307	858	1115	1154	1434	01	01	01	01	01	01	01	01
HPM1 8226				246				34425	01	01	309	567	1614	134	222	60	01	01	01	01	01	01	01	01
ASA/ATCC				247				36516	01	01	685	01	01	153	612	401	01	01	01	01	01	01	01	01
SR				248				19986	01	1351	01	354	733	01	897	62	01	01	01	01	01	01	01	01
OVCA-3				249				27443	307	01	684	852	1417	284	305	266	01	01	01	01	01	01	01	01
MCY-15				250				34819	01	5278	813	1696	2395	1074	208	01	01	01	01	01	01	01	01	01
OVCA-4				251				10333	4781	1077	01	157	587	01	718	01	01	01	01	01	01	01	01	01
UG-31				252				13456	01	415	01	242	757	01	01	116	01	01	01	01	01	01	01	01
OVCA-5				253				50292	01	3782	1757	584	7068	535	102	271	01	01	01	01	01	01	01	01
SN12C				254				39550	119	3368	01	204	43	01	01	01	01	01	01	01	01	01	01	01
OVCA-6				255				16467	159	573	582	512	215	819	104	01	01	01	01	01	01	01	01	01
LOX IMVI				256				45485	01	18604	01	784	8133	01	278	699	01	01	01	01	01	01	01	01
GRV1				257				36126	121	290	760	01	373	1340	360	208	01	01	01	01	01	01	01	01
SK-MEL-2				258				34735	7371	299	1017	01	536	377	73	01	01	01	01	01	01	01	01	01
SK-OV-3				259				17122	2627	01	01	312	584	01	151	118	01	01	01	01	01	01	01	01
SK-MEL-5				260				13827	212	808	01	141	339	01	54	01	01	01	01	01	01	01	01	01
SK-MEL-28				261				38511	656	1771	853	3468	01	858	408	01	01	01	01	01	01	01	01	01
K-562				262				34495	01	337	617	1130	2525	01	262	01	01	01	01	01	01	01	01	01
UACC-257				263				30125	198	11139	01	179	2859	508	55	336	01	01	01	01	01	01	01	01
MYC				264				25143	164	01	606	210	617	97	612	01	01	01	01	01	01	01	01	01
MC7				265				10129	48	01	116	34	278	01	01	01	01	01	01	01	01	01	01	01
MDA-MB-435				267				68935	01	2893	499	607	1409	2558	440	583	01	01	01	01	01	01	01	01
MDA-MB-435				269				26815	01	878	815	40	503	51	01	01	01	01	01	01	01	01	01	01
MDA-MB-435				270				38490	01	01	550	7537	01	416	1472	276	01	01	01	01	01	01	01	01
MDA-MB-435				271				37514	727	703	01	482	213	01	625	01	01	01	01	01	01	01	01	01
Y79 poly A+				273				102505	872	2309	01	922	698	534	1356	01	01	01	01	01	01	01	01	01
KHOS poly A+				280				38001	44	01	8054	8293	4347	3093	1471	01	01	01	01	01	01	01	01	01
HTB36 24h TPA RNA 5/23				300				47107	01	01	550	3518	01	511	387	01	01	01	01	01	01	01	01	01
HELA 62P Q1095				313				18329	01	01	01	01	311	290	01	01	01	01	01	01	01	01	01	01
HTB36 0h RNA				312				52868	109	01	7168	17280	2781	1124	503	01	01	01	01	01	01	01	01	01
HT347				323				40870	186	787	265	18626	01	1252	13	01	01	01	01	01	01	01	01	01
458 melanoma RNA				324				56296	01	01	18772	5011	01	840	363	01	01	01	01	01	01	01	01	01
NCI-H226				326				28074	01	164	752	01	334	408	118	583	01	01	01	01	01	01	01	01
HOP-42				337				15694	01	167	1036	1027	2363	1532	731	01	01	01	01	01	01	01	01	01
MDA-MB-231				338				35092	01	8843	45452	11567	18823	5581	18381	1619	01	01	01	01	01	01	01	01
U251				339				33056	01	19599	13847	7782	83609	10227	10711	5160	01	01	01	01	01	01	01	01
PT cells poly A+				340				11067	71	166	01	1433	01	01	01	01	01	01	01	01	01	01	01	01
PC-3				341				23466	136	283	3486	925	813	386	01	262	01	01	01	01	01	01	01	01
HCC-2998				343				17789	01	501	1731	774	355	873	29	423	01	01	01	01	01	01	01	01
SW 620				345				15302	01	818	1363	589	203	451	1336	643	01	01	01	01	01	01	01	01
HT18				346				42880	87	01	281	1736	2232	1465	01	73	01	01	01	01	01	01	01	01
CCL 205				347				12549	01	01	2285	01	109	01	757	01	01	01	01	01	01	01	01	01
HT218				348				76025	01	01	383	8440	01	01	01	01	01	01	01	01	01	01	01	01
HM-12				349				21716	01	1595	2179	779	350	01	531	349	01	01	01	01	01	01	01	01
HT151				350				24568	89															

Table 3 (cont'd)

Tissue	Tumor sym	Normal sym	Tumor - la	Tumor code	Normal	Endo	p33	SEQ 04	TREQ 43	AA SEQ 47	AA SEQ 48	AA SEQ 49	ANSEQ 51	KUSeq 32	ANSEQ 34	CQSEQ 35	CS
DufPang-2								85383	518	729	0	0	0	0	0	0	0
DufPang-6								26499	248	374	0	0	0	0	0	0	0
DufPang-9								44303	716	156	0	0	0	0	0	0	0
DufPang-11								26981	0	628	0	0	0	0	0	0	0
DufPang-12								05743	0	495	0	0	0	0	0	0	0
DufPang-10								20110	284	211	0	0	0	0	0	0	0
DufPang-1								7684	564	23	0	0	0	0	0	0	0
DufPang-2								2139	281	34	0	0	0	0	0	0	0
DufPang-3								696	1703	265	0	0	0	0	0	0	0
DufPang-4								26952	324	0	0	0	0	0	0	0	0
DufPang-5								32000	0	511	0	0	0	0	0	0	0
DufPang-6								1956	23	90	0	0	0	0	0	0	0
A549 - 8								958	212	0	0	0	0	0	0	0	0
EKVX - 8								0	722	0	0	0	0	0	0	0	0
HCT-116 - 7								171	122	55	0	0	0	0	0	0	0
HCT-116 - 8								310	0	144	0	0	0	0	0	0	0
HT29 - 1								0	0	25	0	0	0	0	0	0	0
HT29 - 7								0	0	51	0	0	0	0	0	0	0
HT29 - 8								1397	36	0	0	0	0	0	0	0	0
SF539 - 7								3320	71	130	0	0	0	0	0	0	0
SF539 - 8								17076	862	0	0	0	0	0	0	0	0
SF-268-7								15222	32	116	0	0	0	0	0	0	0
SF-268-8								12331	29	0	0	0	0	0	0	0	0
OVCAR-4 - 7								12784	4	175	0	0	0	0	0	0	0
OVCAR-4 - 8								4732	0	0	0	0	0	0	0	0	0
OVCAR-5 - 7								3132	0	4	0	0	0	0	0	0	0
OVCAR-5 - 8								3375	440	0	0	0	0	0	0	0	0
MCF-7 - 6								635	0	0	0	0	0	0	0	0	0
ADR-RES - 8								HPV E6	1097	89	0	0	0	0	0	0	0
HeLa - 8								1922	717	22	0	0	0	0	0	0	0
SW480 - 7								412	0	724	0	0	0	0	0	0	0
SW480 - 8								0	162	10	0	0	0	0	0	0	0
HT29S - 8								0	725	4	0	0	0	0	0	0	0
C33A - 7								444	0	0	0	0	0	0	0	0	0
C33A - 8								28619	148	84	0	0	0	0	0	0	0
UZOS - 7								4758	418	0	0	0	0	0	0	0	0

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Table 3 (cont'd)

Tissue	Tumor size	Normal size	Tumor size	Tumor cells	Normal	Endos	p3	SEQ 36	AA	SEQ 37	WT	SEQ 40	AA	SEQ 43	WT	SEQ 44	CA	SEQ 48	HR	SEQ 50	WT	HR	SEQ 51	WT	HR	SEQ 52	WT	HR	SEQ 53	WT	HR	SEQ 54	WT	HR	SEQ 55	WT	HR	SEQ 56	WT	HR	SEQ 57	WT	HR	SEQ 58	WT	HR	SEQ 59	WT	HR	SEQ 60	WT	HR	SEQ 61	WT	HR	SEQ 62	WT	HR	SEQ 63	WT	HR	SEQ 64	WT	HR	SEQ 65	WT	HR	SEQ 66	WT	HR	SEQ 67	WT	HR	SEQ 68	WT	HR	SEQ 69	WT	HR	SEQ 70	WT	HR	SEQ 71	WT	HR	SEQ 72	WT	HR	SEQ 73	WT	HR	SEQ 74	WT	HR	SEQ 75	WT	HR	SEQ 76	WT	HR	SEQ 77	WT	HR	SEQ 78	WT	HR	SEQ 79	WT	HR	SEQ 80	WT	HR	SEQ 81	WT	HR	SEQ 82	WT	HR	SEQ 83	WT	HR	SEQ 84	WT	HR	SEQ 85	WT	HR	SEQ 86	WT	HR	SEQ 87	WT	HR	SEQ 88	WT	HR	SEQ 89	WT	HR	SEQ 90	WT	HR	SEQ 91	WT	HR	SEQ 92	WT	HR	SEQ 93	WT	HR	SEQ 94	WT	HR	SEQ 95	WT	HR	SEQ 96	WT	HR	SEQ 97	WT	HR	SEQ 98	WT	HR	SEQ 99	WT	HR	SEQ 100	WT	HR	SEQ 101	WT	HR	SEQ 102	WT	HR	SEQ 103	WT	HR	SEQ 104	WT	HR	SEQ 105	WT	HR	SEQ 106	WT	HR	SEQ 107	WT	HR	SEQ 108	WT	HR	SEQ 109	WT	HR	SEQ 110	WT	HR	SEQ 111	WT	HR	SEQ 112	WT	HR	SEQ 113	WT	HR	SEQ 114	WT	HR	SEQ 115	WT	HR	SEQ 116	WT	HR	SEQ 117	WT	HR	SEQ 118	WT	HR	SEQ 119	WT	HR	SEQ 120	WT	HR	SEQ 121	WT	HR	SEQ 122	WT	HR	SEQ 123	WT	HR	SEQ 124	WT	HR	SEQ 125	WT	HR	SEQ 126	WT	HR	SEQ 127	WT	HR	SEQ 128	WT	HR	SEQ 129	WT	HR	SEQ 130	WT	HR	SEQ 131	WT	HR	SEQ 132	WT	HR	SEQ 133	WT	HR	SEQ 134	WT	HR	SEQ 135	WT	HR	SEQ 136	WT	HR	SEQ 137	WT	HR	SEQ 138	WT	HR	SEQ 139	WT	HR	SEQ 140	WT	HR	SEQ 141	WT	HR	SEQ 142	WT	HR	SEQ 143	WT	HR	SEQ 144	WT	HR	SEQ 145	WT	HR	SEQ 146	WT	HR	SEQ 147	WT	HR	SEQ 148	WT	HR	SEQ 149	WT	HR	SEQ 150	WT	HR	SEQ 151	WT	HR	SEQ 152	WT	HR	SEQ 153	WT	HR	SEQ 154	WT	HR	SEQ 155	WT	HR	SEQ 156	WT	HR	SEQ 157	WT	HR	SEQ 158	WT	HR	SEQ 159	WT	HR	SEQ 160	WT	HR	SEQ 161	WT	HR	SEQ 162	WT	HR	SEQ 163	WT	HR	SEQ 164	WT	HR	SEQ 165	WT	HR	SEQ 166	WT	HR	SEQ 167	WT	HR	SEQ 168	WT	HR	SEQ 169	WT	HR	SEQ 170	WT	HR	SEQ 171	WT	HR	SEQ 172	WT	HR	SEQ 173	WT	HR	SEQ 174	WT	HR	SEQ 175	WT	HR	SEQ 176	WT	HR	SEQ 177	WT	HR	SEQ 178	WT	HR	SEQ 179	WT	HR	SEQ 180	WT	HR	SEQ 181	WT	HR	SEQ 182	WT	HR	SEQ 183	WT	HR	SEQ 184	WT	HR	SEQ 185	WT	HR	SEQ 186	WT	HR	SEQ 187	WT	HR	SEQ 188	WT	HR	SEQ 189	WT	HR	SEQ 190	WT	HR	SEQ 191	WT	HR	SEQ 192	WT	HR	SEQ 193	WT	HR	SEQ 194	WT	HR	SEQ 195	WT	HR	SEQ 196	WT	HR	SEQ 197	WT	HR	SEQ 198	WT	HR	SEQ 199	WT	HR	SEQ 200	WT	HR	SEQ 201	WT	HR	SEQ 202	WT	HR	SEQ 203	WT	HR	SEQ 204	WT	HR	SEQ 205	WT	HR	SEQ 206	WT	HR	SEQ 207	WT	HR	SEQ 208	WT	HR	SEQ 209	WT	HR	SEQ 210	WT	HR	SEQ 211	WT	HR	SEQ 212	WT	HR	SEQ 213	WT	HR	SEQ 214	WT	HR	SEQ 215	WT	HR	SEQ 216	WT	HR	SEQ 217	WT	HR	SEQ 218	WT	HR	SEQ 219	WT	HR	SEQ 220	WT	HR	SEQ 221	WT	HR	SEQ 222	WT	HR	SEQ 223	WT	HR	SEQ 224	WT	HR	SEQ 225	WT	HR	SEQ 226	WT	HR	SEQ 227	WT	HR	SEQ 228	WT	HR	SEQ 229	WT	HR	SEQ 230	WT	HR	SEQ 231	WT	HR	SEQ 232	WT	HR	SEQ 233	WT	HR	SEQ 234	WT	HR	SEQ 235	WT	HR	SEQ 236	WT	HR	SEQ 237	WT	HR	SEQ 238	WT	HR	SEQ 239	WT	HR	SEQ 240	WT	HR	SEQ 241	WT	HR	SEQ 242	WT	HR	SEQ 243	WT	HR	SEQ 244	WT	HR	SEQ 245	WT	HR	SEQ 246	WT	HR	SEQ 247	WT	HR	SEQ 248	WT	HR	SEQ 249	WT	HR	SEQ 250	WT	HR	SEQ 251	WT	HR	SEQ 252	WT	HR	SEQ 253	WT	HR	SEQ 254	WT	HR	SEQ 255	WT	HR	SEQ 256	WT	HR	SEQ 257	WT	HR	SEQ 258	WT	HR	SEQ 259	WT	HR	SEQ 260	WT	HR	SEQ 261	WT	HR	SEQ 262	WT	HR	SEQ 263	WT	HR	SEQ 264	WT	HR	SEQ 265	WT	HR	SEQ 266	WT	HR	SEQ 267	WT	HR	SEQ 268	WT	HR	SEQ 269	WT	HR	SEQ 270	WT	HR	SEQ 271	WT	HR	SEQ 272	WT	HR	SEQ 273	WT	HR	SEQ 274	WT	HR	SEQ 275	WT	HR	SEQ 276	WT	HR	SEQ 277	WT	HR	SEQ 278	WT	HR	SEQ 279	WT	HR	SEQ 280	WT	HR	SEQ 281	WT	HR	SEQ 282	WT	HR	SEQ 283	WT	HR	SEQ 284	WT	HR	SEQ 285	WT	HR	SEQ 286	WT	HR	SEQ 287	WT	HR	SEQ 288	WT	HR	SEQ 289	WT	HR	SEQ 290	WT	HR	SEQ 291	WT	HR	SEQ 292	WT	HR	SEQ 293	WT	HR	SEQ 294	WT	HR	SEQ 295	WT	HR	SEQ 296	WT	HR	SEQ 297	WT	HR	SEQ 298	WT	HR	SEQ 299	WT	HR	SEQ 300	WT	HR	SEQ 301	WT	HR	SEQ 302	WT	HR	SEQ 303	WT	HR	SEQ 304	WT	HR	SEQ 305	WT	HR	SEQ 306	WT	HR	SEQ 307	WT	HR	SEQ 308	WT	HR	SEQ 309	WT	HR	SEQ 310	WT	HR	SEQ 311	WT	HR	SEQ 312	WT	HR	SEQ 313	WT	HR	SEQ 314	WT	HR	SEQ 315	WT	HR	SEQ 316	WT	HR	SEQ 317	WT	HR	SEQ 318	WT	HR	SEQ 319	WT	HR	SEQ 320	WT	HR	SEQ 321	WT	HR	SEQ 322	WT	HR	SEQ 323	WT	HR	SEQ 324	WT	HR	SEQ 325	WT	HR	SEQ 326	WT	HR	SEQ 327	WT	HR	SEQ 328	WT	HR	SEQ 329	WT	HR	SEQ 330	WT	HR	SEQ 331	WT	HR	SEQ 332	WT	HR	SEQ 333	WT	HR	SEQ 334	WT	HR	SEQ 335	WT	HR	SEQ 336	WT	HR	SEQ 337	WT	HR	SEQ 338	WT	HR	SEQ 339	WT	HR	SEQ 340	WT	HR	SEQ 341	WT	HR	SEQ 342	WT	HR	SEQ 343	WT	HR	SEQ 344	WT	HR	SEQ 345	WT	HR	SEQ 346	WT	HR	SEQ 347	WT	HR	SEQ 348	WT	HR	SEQ 349	WT	HR	SEQ 350	WT	HR	SEQ 351	WT	HR	SEQ 352	WT	HR	SEQ 353	WT	HR	SEQ 354	WT	HR	SEQ 355	WT	HR	SEQ 356	WT	HR	SEQ 357	WT	HR	SEQ 358	WT	HR	SEQ 359	WT	HR	SEQ 360	WT	HR	SEQ 361	WT	HR	SEQ 362	WT	HR	SEQ 363	WT	HR	SEQ 364	WT	HR	SEQ 365	WT	HR	SEQ 366	WT	HR	SEQ 367	WT	HR	SEQ 368	WT	HR	SEQ 369	WT	HR	SEQ 370	WT	HR	SEQ 371	WT	HR	SEQ 372	WT	HR	SEQ 373	WT	HR	SEQ 374	WT	HR	SEQ 375	WT	HR	SEQ 376	WT	HR	SEQ 377	WT	HR	SEQ 378	WT	HR	SEQ 379	WT	HR	SEQ 380	WT	HR	SEQ 381	WT	HR	SEQ 382	WT	HR	SEQ 383	WT	HR	SEQ 384	WT	HR	SEQ 385	WT	HR	SEQ 386	WT	HR	SEQ 387	WT	HR	SEQ 388	WT	HR	SEQ 389	WT	HR	SEQ 390	WT	HR	SEQ 391	WT	HR	SEQ 392	WT	HR	SEQ 393	WT	HR	SEQ 394	WT	HR	SEQ 395	WT	HR	SEQ 396	WT	HR	SEQ 397	WT	HR	SEQ 398	WT	HR	SEQ 399	WT	HR	SEQ 400	WT	HR	SEQ 401	WT	HR	SEQ 402	WT	HR	SEQ 403	WT	HR	SEQ 404	WT	HR	SEQ 405	WT	HR	SEQ 406	WT	HR	SEQ 407	WT	HR	SEQ 408	WT	HR	SEQ 409	WT	HR	SEQ 410	WT	HR	SEQ 411	WT	HR	SEQ 412	WT	HR	SEQ 413	WT	HR	SEQ 414	WT	HR	SEQ 415	WT	HR	SEQ 416	WT	HR	SEQ 417	WT	HR	SEQ 418	WT	HR	SEQ 419	WT	HR	SEQ 420	WT	HR	SEQ 421	WT	HR	SEQ 422	WT	HR	SEQ 423	WT	HR	SEQ 424	WT	HR	SEQ 425	WT	HR	SEQ 426	WT	HR	SEQ 427	WT	HR	SEQ 428	WT	HR	SEQ 429	WT	HR	SEQ 430	WT	HR	SEQ 431	WT	HR	SEQ 432	WT	HR	SEQ 433	WT	HR	SEQ 434	WT	HR	SEQ 435	WT	HR	SEQ 436	WT	HR	SEQ 437	WT	HR	SEQ 438	WT	HR	SEQ 439	WT	HR	SEQ 440	WT	HR	SEQ 441	WT	HR	SEQ 442	WT	HR	SEQ 443	WT	HR	SEQ 444	WT	HR	SEQ 445	WT	HR	SEQ 446	WT	HR	SEQ 447	WT	HR	SEQ 448	WT	HR	SEQ 449	WT	HR	SEQ 450	WT	HR	SEQ 451	WT	HR	SEQ 452	WT	HR	SEQ 453	WT	HR	SEQ 454	WT	HR	SEQ 455	WT	HR	SEQ 456	WT	HR	SEQ 457	WT	HR	SEQ 458	WT	HR	SEQ 459	WT	HR	SEQ 460	WT	HR	SEQ 461	WT	HR	SEQ 462	WT	HR	SEQ 463	WT	HR	SEQ 464	WT	HR	SEQ 465	WT	HR	SEQ 466	WT	HR	SEQ 467	WT	HR	SEQ 468	WT	HR	SEQ 469	WT	HR	SEQ 470	WT	HR	SEQ 471	WT	HR	SEQ 472	WT	HR	SEQ 473	WT	HR	SEQ 474	WT	HR	SEQ 475	WT	HR	SEQ 476	WT	HR	SEQ 477	WT	HR	SEQ 478	WT	HR	SEQ 479	WT	HR	SEQ 480	WT	HR	SEQ 481	WT	HR	SEQ 482	WT	HR	SEQ 483	WT	HR	SEQ 484	WT	HR	SEQ 485	WT	HR	SEQ 486	WT	HR	SEQ 487	WT	HR	SEQ 488	WT	HR	SEQ 489	WT	HR	SEQ 490	WT	HR	SEQ 491	WT	HR	SEQ 492	WT	HR	SEQ 493	WT	HR	SEQ 494	WT	HR	SEQ 495	WT	HR	SEQ 496	WT	HR	SEQ 497	WT	HR	SEQ 498	WT	HR	SEQ 499	WT	HR	SEQ 500	WT	HR	SEQ 501	WT	HR	SEQ 502	WT	HR	SEQ 503	WT	HR	SEQ 504	WT	HR	SEQ 505	WT	HR	SEQ 506	WT	HR	SEQ 507	WT	HR	SEQ 508	WT	HR	SEQ 509	WT	HR	SEQ 510	WT	HR	SEQ 511	WT	HR	SEQ 512	WT	HR	SEQ 513	WT	HR	SEQ 514	WT	HR	SEQ 515	WT	HR	SEQ 516	WT	HR	SEQ 517	WT	HR	SEQ 518	WT	HR	SEQ 519	WT	HR	SEQ 520	WT	HR	SEQ 521	WT	HR	SEQ 522	WT	HR	SEQ 523	WT	HR	SEQ 524	WT	HR	SEQ 525	WT	HR	SEQ 526	WT	HR	SEQ 527	WT	HR	SEQ 528	WT	HR	SEQ 529	WT	HR	SEQ 530	WT	HR	SEQ 531	WT	HR	SEQ 532	WT	HR	SEQ 533	WT	HR	SEQ 534	WT	HR	SEQ 535	WT	HR	SEQ 536	WT	HR	SEQ 537	WT	HR	SEQ 538	WT	HR	SEQ 539	WT	HR	SEQ 540	WT	HR	SEQ 541	WT	HR	SEQ 542	WT	HR	SEQ 543	WT	HR	SEQ 544	WT	HR	SEQ 545	WT	HR	SEQ 546	WT	HR	SEQ 547	WT	HR	SEQ 548	WT	HR	SEQ 549	WT	HR	SEQ 550	WT	HR	SEQ 551	WT	HR	SEQ 552	WT	HR	SEQ 553	WT	HR	SEQ 554	WT	HR	SEQ 555	WT	HR	SEQ 556	WT	HR	SEQ 557	WT	HR	SEQ 558	WT	HR	SEQ 559	WT	HR	SEQ 560	WT	HR	SEQ 561	WT	HR	SEQ 562	WT	HR	SEQ 563	WT	HR	SEQ 564	WT	HR	SEQ 565	WT	HR	SEQ 566	WT	HR	SEQ 567	WT	HR	SEQ 568	WT	HR	SEQ 569	WT	HR	SEQ 570	WT	HR	SEQ 571	WT	HR	SEQ 572	WT	HR	SEQ 573	WT	HR	SEQ 574	WT	HR	SEQ 575	WT	HR	SEQ 576	WT	HR	SEQ 577	WT	HR	SEQ 578	WT	HR	SEQ 579	WT	HR	SEQ 580	WT	HR	SEQ 581	WT	HR	SEQ 582	WT	HR	SEQ 583	WT	HR	SEQ 584	WT	HR	SEQ 585	WT	HR	SEQ 586	WT	HR	SEQ 587	WT	HR	SEQ 588	WT	HR	SEQ 589	WT	HR	SEQ 590	WT	HR	SEQ 591	WT	HR	SEQ 592	WT	HR	SEQ 593	WT	HR	SEQ 594	WT	HR	SEQ 595	WT	HR	SEQ 596	WT	HR	SEQ 597	WT	HR	SEQ 598	WT	HR	SEQ 599	WT	HR	SEQ 600	WT	HR	SEQ 601	WT	HR	SEQ 602	WT	HR	SEQ 603	WT	HR	SEQ 604	WT	HR	SEQ 605	WT	HR	SEQ 606	WT	HR	SEQ 607	WT	HR	SEQ 608
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Table 3 (cont'd)

Tissue	Tumor g/m	Normal g/m	Tumor % to	Tumor cells	Normal	Endo	#3	SEQ 17	AA	SEQ 20	SEQ 22	PT	SEQ 24	AA	SEQ 29	OR	SEQ 31	OR	SEQ 32	AA	SEQ 40	AA	SEQ 44	1
Ha-5181	153							46043	1431	111614	7206	23561	8371	93451	01	369								
MGF-1A/DR-RES	153							46543	01	704111	7211	3871	0	155591	01	829								
MGF-7	151							53449	94	30604	11824	20501	218	138251	01	0								
M14	147							63303	3711	22226	14925	2725	257	4104	915	73								
UACG-757	149							36000	10931	72538	4016	1111	0	32383	0	311								
UACG-69	145							27441	01	7696	3021	9961	741	96001	206	251								
SK-MEL-20	144							20951	711	10249	14021	2016	634	40671	1161	264								
UO-31	143							56230	0	12453	3316	844	1206	1627	1685	0								
SK-MEL-5	142							29301	0	137876	16621	110	260	18600	490	134								
KM-12	141							30992	297	8923	2025	5	65	1261	0	329								
SK-MEL-2	140							30577	0	58284	3528	9271	495	19563	0	188								
HCT-15	139							54729	445	25281	2709	15721	287	8966	542	0								
MeMe-3M	138							45060	1466	86469	4322	243	294	12794	226	451								
COLO-205	137							57736	433	16962	2580	486	0	5756	0	174								
LOX IMV1	136							29210	0	161759	1512	660	567	26226	214	628								
SW-620	135							28849	432	29529	750	203	186	9406	375	166								
TK-10	134							43297	68	18978	1719	683	262	7065	72	45								
HCT-116	133							37409	345	18726	1178	0	458	3812	721	68								
TR60	132							24175	0	27523	0	534	157	6539	567	14								
HCC-2998	131							42262	329	17250	0	159	238	3661	0	541								
ACHN	130							28600	329	91730	1353	617	303	10449	25	226								
PC-3	129							35262	33	50087	1005	106	457	8755	519	0								
PCP-203	128							40444	305	82661	3146	2477	2041	26924	478	0								
DL-145	127							37277	0	8182	5151	140	400	15854	0	0								
Cal-1	126							35257	331	51153	9431	95	527	22788	506	190								
SR	125							37859	0	50238	7507	1172	551	26608	156	0								
A498	124							39184	0	106212	4214	0	1685	2925	423	666								
RPMI 8226	123							50465	237	6134	28001	2182	317	13014	0	0								
SN12C	122							32576	95	44777	536	1473	150	23039	0	537								
K-60	121							36440	566	2018	0	325	771	707	86	380								
MEL-14	120							28209	782	17195	881	532	1023	4039	0	0								
OVCA-5	119							25375	0	43226	1596	327	222	5444	0	77								
K-562	118							54213	582	18149	2128	367	222	5444	0	0								
OVCA-4	117							42508	1500	108942	5120	2239	2583	8251	1228	1110								
CEBPG-CEM	116							36120	576	100622	2781	631	4767	41562	0	0								
OVCA-3	115							52071	548	47693	1247	969	307	10248	2443	0								
SF-539	114							34665	86	14022	2625	0	350	10293	0	252								
HOP-62	113							19516	0	64930	1645	1194	665	7728	0	100								
SF-295	112							40830	257	17908	700	708	1164	5386	417	631								
AS49ATCC	111							47438	0	78178	1610	496	303	17019	1514	572								
SF-268	110							30245	64	56467	972	185	76	13647	482	568								
NCI-H522	109							44511	0	81026	965	813	276	6039	0	94								
U251	108							54076	433	46759	573	124	718	11977	86	0								
NCI-H660	107							28965	256	75128	436	405	807	17566	809	152								
SNB-75	106							41104	0	17012	403	456	369	4792	884	316								
NCI-H522M	105							49937	69	10250	3058	4827	461	26339	746	0								
SNB-19	104							50554	442	13625	1417	451	2644	32654	156	625								
NCI-H226	103							41587	533	8672	3208	1331	806	18328	743	69								
SK-OV-3	102							33170	0	18596	3041	522	200	18091	243	61								
NCI-H460	101							30481	0	5614	4702	140	203	29997	0	491								
IGROV1	100							41669	442	11790	2691	229	203	13118	0	0								
EKVE	99							25817	0	14573	1622	0	442	34177	0	0								
OVCA-8	98							31129	0	7823	48	101	197	9392	11	0								
HOP-62	97							33300	0	10562	1074	366	465	12792	452	103								
n. sub. SMC 10/2 V02 #12	47							12090	0	8172	1598	5270	341	401	200	184								
n. sub. SMC 10/2 V02 #17	46							20917	185	1285	0	150	0	963	127	0								
n. sub. SMC 10/2 V02 #10	26							29128	66	23461	1117	0	92	10270	344	0								
TCOP	25							22553	700	18108	7310	86	120	5277	1704	111								
A549 - 1	0							mutant	0	0	0	349	4138	4388	413	571	0							
A549 - 3	0							mutant	0	0	0	6311	124	4678	539	1033	0							
A549 - 4	0							mutant	0	0	0	0	1294	7899	0	880	0							
A549 - 5	0							mutant	0	0	0	0	458	6066	143	0	0							
A549 - 7	0							mutant	0	0	0	0	813	5974	787	0	0							
EKVE - 1	0							mutant	0	0	0	1340	3420	6820	475	2339	0							
EKVE - 3	0							mutant	0	0	0	2006	4210	10881	330	180	0							
EKVE - 4	0							mutant	0	0	0	1809	0	4661	0	705	0							
EKVE - 5	0							mutant	0	0	0	294	1113	5687	137	0	0							
EKVE - 7	0							mutant	0	0	0	0	37	7403	867	0	0							
MGF-7 - 1	0							mutant	0	0	0	453	801	110	3344	155	0							
MGF-7 - 3	0							mutant	0	0	0	16	1048	2997	0	492	0							
MGF-7 - 4	0							mutant	0	0	0	815	927	1029	211	1366	0							
MGF-7 - 5	0							mutant	0	0	0	1181	2631	4029	0	888	0							
MGF-7 - 7	0							mutant	0	0	0	0	590	433	607	629	0							
ADR-RES - 1	0							mutant	0	0	0	0	2736	2787	4698	2088	0							
ADR-RES - 3	0							mutant	0	0	0	1148	3462	4039	1056	8	0							
ADR-RES - 4	0							mutant	0	0	0	112	0	2817	637	601	0							
ADR-RES - 5	0							mutant	0	0	0	403	2399	852	0	0	0							
ADR-RES - 7	0							mutant	0	0	0	2011	2696	1855	896	496	0							
WI 30 - 1	0							mutant	0	0	0	0	7756	3646	589	1631	0							

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - to	Tumor cells	Normal	Endo	p53	SEQ 17 AA	SEQ 20 SC	SEQ 22 PT	SEQ 26 AA	SEQ 29 DR	SEQ 31 DR	SEQ 32 AK	SEQ 48 M	SEQ 64 T
Dafeng-7								0	0	0	216941	8478	315501	27281	1224	0
Dafeng-8								0	0	0	10605	85431	17854	1690	10781	0
Dafeng-9								0	0	0	9122	15881	259731	1318	544	0
Dafeng-11								0	0	0	7501	9216	14351	1857	969	0
Dafeng-12								0	0	0	3497	3288	16748	1028	0	0
Dafeng-10								0	0	0	6482	256	19429	311	210	0
Dafeng-1								0	0	0	3541	12536	1787	831	11952	0
Dafeng-2								0	0	0	3679	10369	6327	148	69625	0
Dafeng-3								0	0	0	4784	2945	2782	3207	4773	0
Dafeng-4								0	0	0	1944	4731	97	4214	903	0
Dafeng-5								0	0	0	1170	2029	321	1817	2183	0
Dafeng-6								0	0	0	12057	5346	0	2639	1453	0
AS49 - 8							wt	0	0	0	0	1464	8652	0	427	0
EKVI - 8							mutant	0	0	0	1513	2153	6496	560	17	0
HCT-116 - 7							wt	0	0	0	742	2507	3943	5499	618	0
HCT-116 - 8							wt	0	0	0	614	8117	2307	761	0	0
HT29 - 1							mutant	0	0	0	420	3056	3122	691	0	0
HT29 - 7							mutant	0	0	0	444	150	8	0	151	0
HT29 - 8							wt	0	0	0	1051	2900	2178	0	1146	0
SF539 - 7							wt	0	0	0	6143	2843	1075	208	0	0
SF539 - 8							wt	0	0	0	66	10248	2922	562	0	0
SF-268-7							mutant	0	0	0	771	6991	2712	1190	1054	0
SF-268-8							wt	0	0	0	1168	8034	4622	394	0	0
QVCAR-4 - 7							wt	0	0	0	0	1284	6363	0	0	0
QVCAR-4 - 8							wt	0	0	0	2050	2109	13609	593	3736	0
QVCAR-5 - 7							mutant	0	0	0	0	657	21830	0	0	0
QVCAR-5 - 8							wt	0	0	0	89	2853	7100	2593	0	0
MCF-7 - 8							wt	0	0	0	0	2539	1521	0	190	0
ADR-RES - 8							mutant	0	0	0	465	672	3321	0	0	0
HEL - 6							HPV E6	0	0	0	1829	225	4763	1418	0	0
SW480 - 7							mutant	0	0	0	246	841	4842	0	14271	0
SW480 - 8							wt	0	0	0	870	0	4236	0	1166	0
HI299 - 8							mutant	0	0	0	1405	4781	2495	296	49	0
C3A - 7							mutant	0	0	0	0	2052	2718	10023	837	0
C3A - 8							wt	0	0	0	0	0	451	865	0	0
U2OS - 7							mutant	0	0	0	2235	4545	3018	877	1583	0
U2OS - 6							mutant	0	0	0	31	4840	8016	0	0	0
Hs68 - 7							wt	0	0	0	10261	346	3165	144	0	0
Hs68 - 8							wt	0	0	0	1446	1183	3374	1682	0	0
WI 38 - 8							wt	0	0	0	1470	0	3254	0	425	0
45S modulator RNA								0	37668	0	4415	210	299	1447	6182	0
CHL 1572 3/1789								25584	578	738	543	4683	27	579	16	58
Bov-1								59010	0	0	1007	3021	1552	0	336	0
HT368								32554	0	0	7687	21100	3573	29	0	321
HT378								37558	9	386	662	2960	5974	0	0	0
HT385								76812	0	0	14370	8958	1359	316	0	0
HT388								21762	851	0	0	3209	1103	185	673	574
Bov-3								36211	38	0	0	1824	1810	78	178	0
Bov-5								19950	0	0	0	311	60	0	1711	18
Bov-6								39076	0	142	263	0	643	0	418	110
h. sw. drosophila 3/2592 #10								50327	0	0	3949	556	49	0	1798	0
Bov-10								45182	237	245	131	2244	400	0	123	0
HTB10								86289	0	0	1379	3593	0	0	0	0
prostate 8								44374	88	0	0	4810	78	0	261	0
MINO-OG poly A+								29035	7	0	0	5462	14	0	0	0
SA-OS (pAundly) poly A+								24676	236	1073	3362	3701	1721	1048	0	0
MCF poly A+								27097	0	0	10768	5681	674	0	0	0
HCT-116 - 3							wt	32124	0	261	12603	10412	478	1862	863	483
HCT-116 - 4							wt	0	0	0	1768	4484	297	24	0	0
HCT-116 - 5							wt	0	0	0	3318	7870	113	0	0	0
HCT-116 - 6							wt	0	0	0	3783	1899	3247	0	0	0
AS49 - 6							wt	0	0	0	508	2679	7618	267	246	0
EKVI - 6							wt	0	0	0	0	2201	52	0	302	0
HT29 - 3							mutant	0	0	0	148	4624	7875	1143	513	0
HT29 - 4							mutant	0	0	0	0	1949	2376	0	435	0
HT29 - 5							mutant	0	0	0	1235	323	3234	181	0	0
HT29 - 6							mutant	0	0	0	1070	3696	3647	0	363	0
QVCAR-4 - 3							wt	0	0	0	2050	5879	800	0	0	0
QVCAR-4 - 4							wt	0	0	0	1203	1613	11856	870	1055	0
QVCAR-4 - 5							wt	0	0	0	0	708	8721	0	669	0
QVCAR-4 - 6							wt	0	0	0	899	3034	13755	1753	3849	0
SF539 - 3							wt	0	0	0	613	18879	2575	211	264	0
SF539 - 4							wt	0	0	0	1208	4103	1672	156	746	0
SF539 - 5							wt	0	0	0	0	1893	3256	0	109	0
SF539 - 6							wt	0	0	0	946	1292	2380	414	0	0
SF539 - 7							wt	0	0	0	549	5490	0	540	908	0
QVCAR-5 - 3							mutant	0	0	0	1547	6497	7120	0	111	0
QVCAR-5 - 4							mutant	0	0	0	0	3700	2419	28	400	0
QVCAR-5 - 5							mutant	0	0	0	236	368	1633	43	0	0
ADR-RES - 6							wt	0	0	0	636	2829	2267	433	0	0
MCF-7 - 6							wt	0	0	0	0	1654	2859	94	718	0
HEL - 6							HPV E6	0	0	0	1327	1684	4791	129	162	0
HI299 - 6							mutant	0	0	0	309	0	322	0	0	0
SW480 - 3							mutant	0	0	0	0	659	3520	783	2908	0
SW480 - 4							mutant	0	0	0	0	377	3979	562	1084	0
SW480 - 5							mutant	0	0	0	2315	1275	4248	380	14325	0
SW480 - 6							mutant	0	0	0	1702	1928	4535	50	1577	0
C3A - 3							mutant	0	0	0	0	0	1963	0	298	0
C3A - 4							mutant	0	0	0	72	775	451	0	608	0
C3A - 5							mutant	0	0	0	0	5487	0	0	0	0
C3A - 6							mutant	0	0	0	0	10	21373	0	0	0
Hs68 - 6							wt	0	0	0	578	41	5471	351	264	0
U2OS - 3							mutant	0	0	0	1430	11036	8621	10083	5153	0
U2OS - 4							mutant	0	0	0	1199	6148	5064	1818	2063	0
U2OS - 5							mutant	0	0	0	1755	6155	2586	0	3700	0
U2OS - 6							mutant	0	0	0	606	17687	518	502	219	0
WI 38 - 6							wt	0	0	0	1629	2318	2548	399	0	0
Hs68 - 3							wt	0	0	0	2401	8407	7121	105	529	0
Hs68 - 4							wt	0	0	0	2780	5182	20959	1617	0	0
SF-268-3							mutant	0	0	0	1194	5180	6451	0	0	0
SF-268-4							mutant	0	0	0	1117	2862	4751	1674	22	0
SF-268-5							mutant	0	0	0	1635	3820	3241	0	0	0
SF-268-6							mutant	0	0	0	1614	4399	84	402	0	0
Dafeng-13								5018	17553	12066	2259	8095	0	0	0	0
Manuel - 20								4071	10817	12558	2887	7190	0	0	0	0
Manuel - 21								2619	4567	7698	589	3397	0	0	0	0
QVCAR-5 - 5							wt	0	0	0	3963	3314	2633	7314	651	0
Manuel - 10							mutant	0	0	0	4563	8671	4413	260	2940	0
Manuel - 11</																

Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - fe	Tumor - cste	Normal	Endoc	p33	SEQ 844	TSEQ 45	AA	SEQ 47	AA	SEQ 48	AA	SEQ 49	AA	SEQ 51	AA	SEQ 52	AA	SEQ 54	AA	SEQ 55	AA
adrenal gland - h	1	1						106241	0	0	207	584	8574	7198	2170	7791	20262	37691						
lymph node - h	2	3						1985	0	237	0	5663	3816	1381	1112	45217								
bone marrow - h	3	4						441	0	0	0	2755	1143	293	0	19793								
pancreatic gland - h	4	5						4681	0	169	230	6495	805	807	11958	31129								
ovary - h	5	6						384	0	0	344	7076	3342	838	8732	44206								
pancreas - h	6	7						8608	0	70	0	7609	2630	3189	13785	85393								
cardiac muscle - h	7	8						10870	0	60	211	8528	6997	9321	3226	36020								
adipose tissue - h	8	9						57149	0	257	89	7243	5614	3007	26437	47438								
testis - h	9	10						1428	0	51	87	8163	2360	2312	41093	35806								
placenta - h	10	11						2337	0	233	0	9334	8433	1375	30344	73605								
testis - h	11	12						2093	0	114	0	7673	3767	354	55511	21151								
testis - h	12	13						2978	0	196	180	8958	1682	810	4385	47110								
testis - h	13	14						0	0	130	0	9005	3418	1128	5531	26923								
salivary gland - h	14	15						6390	0	319	345	10713	6378	1758	20642	64752								
testis - h	15	16						32869	0	0	0	5708	1942	1193	2028	14512								
skel muscle - h	16	17						6442	0	101	101	5123	472	1022	2810	14161								
heart - h	17	18						2753	0	86	144	1037	2965	443	41721	22790								
small intestine - h	18	19						0	0	181	225	6344	2052	261	7039	31645								
kidney - h	19	20						0	0	136	0	5679	2646	558	1254	14331								
spinal cord - h	20	21						8349	0	0	0	4814	0	833	0	15765								
testis - h	21	22						2363	0	0	196	5447	3308	631	997	18460								
spleen - h	22	23						2011	0	105	177	3966	2134	673	3438	24017								
lung - h	23	24						2652	0	125	0	3808	812	281	1243	17607								
stomach - h	24	25						20445	0	1160	290	5639	8751	11864	321718	49517								
testis - h	25	26						1302	0	47	23	6191	4925	1638	11408	85005								
thymus - h	26	27						356	0	35	35	5356	0	0	0	9076								
HPAEC	27	28						805	0	158	0	5306	1800	556	8454	27900								
HPAEC	28	29						3411	0	19	98	4184	10744	64	0	1490								
HPAEC	29	30						188	0	19	98	4184	10744	64	0	1490								
HPAEC	30	31						3411	0	19	98	4184	10744	64	0	1490								
HPAEC	31	32						0	0	35	188	4406	144	99	393	9796								
HPAEC	32	33						3981	0	62	307	7257	7343	1366	7394	36540								
HPAEC	33	34						184	0	26	70	5751	6835	218	661	21419								
HPAEC	34	35						520	0	0	6288	0	0	0	0	0								
HPAEC	35	36						1518	0	116	0	5373	20944	115	9677	25025								
HPAEC	36	37						399	0	14	0	3413	0	31	0	2243								
HPAEC	37	38						8035	0	0	0	6881	8072	134	0	2341								
HPAEC	38	39						0	0	17	33	4065	10004	41	0	2701								
HPAEC	39	40						100	0	0	67	4633	8751	0	0	26456								
HPAEC	40	41						92	0	0	0	3090	0	0	0	2975								
HPAEC	41	42						11823	0	0	0	5653	8784	145	0	18626								
HPAEC	42	43						0	0	407	5511	1427	0	0	0	16266								
HPAEC	43	44						1732	0	27	53	7444	19562	115	12733	22793								
HPAEC	44	45						671	0	0	0	301	0	0	0	0								
HPAEC	45	46						365	0	0	0	225	0	0	0	482								
HPAEC	46	47						363	0	0	0	0	0	0	0	0								
HPAEC	47	48						2198	0	0	47	1307	387	21	0	8452								
HPAEC	48	49						361	0	0	0	403	8650	2907	248	0	6825							
HPAEC	49	50						354	354	6027	0	40	0	6406	346	116	330	2534						
HPAEC	50	51						344	0	0	71	1962	4871	50	360	6728								
HPAEC	51	52						342	0	0	0	1828	1176	0	2981	7542								
HPAEC	52	53						334	334	0	0	200	90401	117	0	0	0							
HPAEC	53	54						332	0	0	61	0	4034	0	521	0	27619							
HPAEC	54	55						330	0	0	0	336	4452	0	87	0	351							
HPAEC	55	56						328	0	0	0	7086	29	603	43501	15417								
HPAEC	56	57						327	0	0	118	176	4857	0	0	42	409							
HPAEC	57	58						326	0	0	0	250	5563	0	625	547	78037							
HPAEC	58	59						321	0	0	0	3459	0	0	0	7102								
HPAEC	59	60						318	0	0	6	3821	0	0	0	3657								
HPAEC	60	61						320	0	0	0	0	0	0	0	0								
HPAEC	61	62						316	0	0	313	0	6339	8543	0	66964								
HPAEC	62	63						314	0	0	29	164	4057	2227	167	5551	22075							
HPAEC	63	64						311	0	0	229	176	5212	4413	343	5888	53830							
HPAEC	64	65						308	0	0	84	0	5050	810	27	0	17721							
HPAEC	65	66						306	0	0	0	5456	708	0	0	11078								
HPAEC	66	67						307	0	0	0	370	2428	0	66	205	5405							
HPAEC	67	68						305	0	0	34	250	8133	2262	58	622	22026							
HPAEC	68	69						303	0	0	362	33	5270	4075	0	0	37185							
HPAEC	69	70						302	0	0	370	104	5051	1673	145	1017	78889							
HPAEC	70	71						300	0	0	233	64	9599	12917	644	2097	67619							
HPAEC	71	72						298	0	0	0	4872	0	44	1583	30392								
HPAEC	72	73						297	0	0	114	0	3615	3035	0	462	38439							
HPAEC	73	74						296	0	0	64	0	5831	2045	304	643	26976							
HPAEC	74	75						294	0	0	0	0	2932	657	176	134	18375							
HPAEC	75	76						292	0	0	86	0	5290	631	58	824	48425							
HPAEC	76	77						290	0	0	245	0	5290	631	58	824	48425							
HPAEC	77	78						288	0	0	88	336	5448	116	0	395	8531							
HPAEC	78	79						277	0	0	0	4734	1192	6	1346	10122								
HPAEC	79	80						275	275	0	41	181	3704	874	83	0	6275							
HPAEC	80	81						266	0	0	7	3652	242	349	0	0	11174							
HPAEC	81	82																						

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - 1g	Tumor cells	Normal	Endos	p33	SEQ 44	TREK	45	AA	SEQ 47	AA	SEQ 48	AA	SEQ 51	MI	SEQ 57	AA	SEQ 54	CC	SEQ 55	CL
CRL-1441 RNA 8/30			166					0	0	0	47	89	40121	0	164	258	5448						
786-9			168					4017	0	0	0	8121	1662	46	0	24521	20085						
T-47D			169					0	0	0	70	212	4456	73	295	65311	7187						
Ken-3			171					0	0	0	75	1645	278	6	0	261							
CRL-1441 RNA 8/30			181					0	0	0	567	12091	120	383	192	0							
T-211 untreated + DNase			183					0	0	0	211	8	867	11	212	419							
K562 poly A+			194					0	0	0	135	1653	24	52	211	7891							
HOS poly A+			196					287	0	0	48	0	2437	0	64	84	3761						
ACHN			198					0	0	0	0	2632	209	171	8142	3184							
UACC-62			200					385	0	0	131	1296	0	0	1272	1373							
MCF-7/ADR-RES			202					0	0	0	36	0	1257	700	0	1430	1028						
UTOS (Mammary) poly A+			204					0	0	0	171	22	0	0	0	9423							
WISH (Gallbladder) poly A+			206					0	0	0	0	742	843	44	42	1191							
458 medullary mDNA			208					5841	0	0	0	7137	0	0	0	8852							
CCL137 RNA 3/21/88			218					0	0	0	80	141	1094	2	109	627							
WI-38 72h 0.5%FBS, 24h 10% FBS			219					0	0	0	0	2120	0	77	0	892							
CRL1441 + TPA (24h) 8/30			220					0	0	0	224	995	93	0	0	0							
Ken-1			221					689	0	0	0	16	1572	0	0	1257							
Ken-2			222					0	0	0	83	15	2225	320	85	0	1981						
Ken-4			225					736	0	0	172	0	2728	0	0	1331							
HOP-92			241					126	0	0	3	1124	372	0	0	1758							
MOLT-4			242					1229	0	0	0	4196	1256	0	2452	5190							
EKVX			243					804	0	0	129	2140	139	217	1440								
HL-60			244					0	0	0	0	3652	507	614	1496	10317							
NCLH23			245					237	0	0	10	163	3528	1613	221	3362	6328						
BTMA B225			246					0	0	0	88	413	2687	7116	162	0	738						
A549ATCC			247					0	0	0	96	0	2255	0	0	1684							
SR			248					0	0	0	0	2109	1910	33	261	2209							
OVCA-3			249					0	0	0	17	267	3481	0	45	1631	544						
HCT-15			250					1042	0	0	0	627	4998	1567	293	648	13641						
OVCA-4			251					63	0	0	83	15	557	17	69	141							
UO-31			252					3471	0	0	0	56	814	0	0	463	1047						
OVCA-5			253					0	0	0	89	722	6152	0	362	47893	6832						
FA13C			254					811	0	0	0	3554	2391	0	10455	6558							
OVCA-8			255					322	0	0	13	872	0	0	210	2742							
LOX IMVI			256					0	0	0	77	343	8201	4994	2250	4100							
IGROV1			257					894	0	0	94	0	3989	571	3	2367	3837						
SK-MEL-2			258					0	0	0	115	0	2345	401	336	1374	2004						
SK-OV-3			259					0	0	0	0	116	0	164	1499	1437							
SK-MEL-5			260					0	0	0	472	1328	199	0	192	1486							
SF-539			261					1273	0	0	166	458	6873	2291	0	7414	2689						
SK-MEL-28			262					857	0	0	0	3750	861	0	2959	2053							
K-562			263					157	0	0	85	31	8148	4346	216	2532	3781						
UACC-257			264					608	0	0	0	2881	0	427	0	1280							
M14			265					0	0	0	74	0	877	151	181	1454							
MCF7			267					5620	0	0	0	26	8238	0	0	17404	29602						
MDA-MB-435			268					60	0	0	231	1824	0	0	74	1243							
HT279			270					1743	0	0	0	1555	2593	67	0	2964							
MDA-N			271					0	0	0	17	0	4127	0	293	1252	2025						
Y79 poly A+			273					8095	0	0	137	0	7232	1899	43	856	16372						
RKHS poly A+			279					2789	0	0	18	269	32	264	578	8284							
HTB36 24h TPA RNA 6/23			300					0	0	0	10	0	2952	546	171	64	6376						
HELIX-EXP-031899			313					0	0	0	19	49	2177	849	24	0	10940						
HTB36 On RNA			332					639	0	0	199	4154	566	428	773	4214							
HT347			333					443	0	0	5	2448	3812	0	169	58352							
458 medullary RNA			334					2299	0	0	55	0	3454	0	11	781	1101						
NCLH226			336					0	0	0	0	38	2966	0	100	0	1149						
HOP-42			337					0	0	0	0	357	3132	301	181	5222	2879						
MDA-MB-231			338					7540	0	0	23	8113	4555	0	8554	26931							
U251			339					10346	0	0	66	0	11556	19310	202	141693	38706						
PT cells poly A+			340					0	0	0	0	0	1866	0	0	2461	2005						
PC-3			341					0	0	0	227	3670	708	83	5841	818							
RCC-2998			343					31	0	0	0	2486	0	139	0	102	6102						
SW-620			345					0	0	0	72	83	2072	0	196	36	0						
HT102			346					578	0	0	50	25	4300	509	0	3475	19731						
CCL-205			347					0	0	0	28	45	703	688	0	0	0						
HT218			348					4311	0	0	0	1703	0	0	0	1855							
RAM-12			349					0	0	0	44	137	1724	842	102	0	1130						
HT151			350					0	0	0	30	202	3787	1543	299	0	8776						
A-498			351					7849	0	0	0	164	1648	0	200	0	0						
HT363			352					225	0	0	0	6001	0	0	0	18118							
RXF-383			353					0	0	0	114	0	2570	0	0	775							
TK-10			355					5344	0	0	0	7558	2225	0	3006	17069							
Mammary-3M			357					2945	0	0	0	0	26180	15570	313	37531	7453						
Ha 5787			359					0	0	0	0	0	1858	0	0	996	6102						
HT213			50					0	0	0	162	0	18523	1275	37	0	4385						
HT258			52					195	0	0	197	0	5482	437	0	429	48348						
HT159			54					0	0	0	31	3241	0	0	0	2708							
HT155			56					0	0	0	114	0	29651	0	0	12742							
HT163			58					337	0	0	35	26	3238	588	0	249							
HT170			60					0	0	0	28	0	6032	0	0	12650							
HT172			62					0	0	0	5	0	4071	0	94	1041	2202						
HT138			63					1383	0	0	0	3571	121	0	0	26749							
HT178			64					0	0	0	201	5024	0	0	0	2861							
HT154			65					1635	0	0	0	6175	1963										

Tumor	sym	Normal	sym	Tumor	iso	Tumor	exile	Normal	Endos	p53	SE0	844	TR00	45	AA	SEQ	47	AA	SEQ	48	AA	SEQ	49	AA	SEQ	50	AA	SEQ	51	AA	SEQ	52	AA	SEQ	53	AA	SEQ	54	AA	SEQ	55	AA	SEQ	56	AA	SEQ	57	AA	SEQ	58	AA	SEQ	59	AA	SEQ	60	AA	SEQ	61	AA	SEQ	62	AA	SEQ	63	AA	SEQ	64	AA	SEQ	65	AA	SEQ	66	AA	SEQ	67	AA	SEQ	68	AA	SEQ	69	AA	SEQ	70	AA	SEQ	71	AA	SEQ	72	AA	SEQ	73	AA	SEQ	74	AA	SEQ	75	AA	SEQ	76	AA	SEQ	77	AA	SEQ	78	AA	SEQ	79	AA	SEQ	80	AA	SEQ	81	AA	SEQ	82	AA	SEQ	83	AA	SEQ	84	AA	SEQ	85	AA	SEQ	86	AA	SEQ	87	AA	SEQ	88	AA	SEQ	89	AA	SEQ	90	AA	SEQ	91	AA	SEQ	92	AA	SEQ	93	AA	SEQ	94	AA	SEQ	95	AA	SEQ	96	AA	SEQ	97	AA	SEQ	98	AA	SEQ	99	AA	SEQ	100	AA	SEQ	101	AA	SEQ	102	AA	SEQ	103	AA	SEQ	104	AA	SEQ	105	AA	SEQ	106	AA	SEQ	107	AA	SEQ	108	AA	SEQ	109	AA	SEQ	110	AA	SEQ	111	AA	SEQ	112	AA	SEQ	113	AA	SEQ	114	AA	SEQ	115	AA	SEQ	116	AA	SEQ	117	AA	SEQ	118	AA	SEQ	119	AA	SEQ	120	AA	SEQ	121	AA	SEQ	122	AA	SEQ	123	AA	SEQ	124	AA	SEQ	125	AA	SEQ	126	AA	SEQ	127	AA	SEQ	128	AA	SEQ	129	AA	SEQ	130	AA	SEQ	131	AA	SEQ	132	AA	SEQ	133	AA	SEQ	134	AA	SEQ	135	AA	SEQ	136	AA	SEQ	137	AA	SEQ	138	AA	SEQ	139	AA	SEQ	140	AA	SEQ	141	AA	SEQ	142	AA	SEQ	143	AA	SEQ	144	AA	SEQ	145	AA	SEQ	146	AA	SEQ	147	AA	SEQ	148	AA	SEQ	149	AA	SEQ	150	AA	SEQ	151	AA	SEQ	152	AA	SEQ	153	AA	SEQ	154	AA	SEQ	155	AA	SEQ	156	AA	SEQ	157	AA	SEQ	158	AA	SEQ	159	AA	SEQ	160	AA	SEQ	161	AA	SEQ	162	AA	SEQ	163	AA	SEQ	164	AA	SEQ	165	AA	SEQ	166	AA	SEQ	167	AA	SEQ	168	AA	SEQ	169	AA	SEQ	170	AA	SEQ	171	AA	SEQ	172	AA	SEQ	173	AA	SEQ	174	AA	SEQ	175	AA	SEQ	176	AA	SEQ	177	AA	SEQ	178	AA	SEQ	179	AA	SEQ	180	AA	SEQ	181	AA	SEQ	182	AA	SEQ	183	AA	SEQ	184	AA	SEQ	185	AA	SEQ	186	AA	SEQ	187	AA	SEQ	188	AA	SEQ	189	AA	SEQ	190	AA	SEQ	191	AA	SEQ	192	AA	SEQ	193	AA	SEQ	194	AA	SEQ	195	AA	SEQ	196	AA	SEQ	197	AA	SEQ	198	AA	SEQ	199	AA	SEQ	200	AA	SEQ	201	AA	SEQ	202	AA	SEQ	203	AA	SEQ	204	AA	SEQ	205	AA	SEQ	206	AA	SEQ	207	AA	SEQ	208	AA	SEQ	209	AA	SEQ	210	AA	SEQ	211	AA	SEQ	212	AA	SEQ	213	AA	SEQ	214	AA	SEQ	215	AA	SEQ	216	AA	SEQ	217	AA	SEQ	218	AA	SEQ	219	AA	SEQ	220	AA	SEQ	221	AA	SEQ	222	AA	SEQ	223	AA	SEQ	224	AA	SEQ	225	AA	SEQ	226	AA	SEQ	227	AA	SEQ	228	AA	SEQ	229	AA	SEQ	230	AA	SEQ	231	AA	SEQ	232	AA	SEQ	233	AA	SEQ	234	AA	SEQ	235	AA	SEQ	236	AA	SEQ	237	AA	SEQ	238	AA	SEQ	239	AA	SEQ	240	AA	SEQ	241	AA	SEQ	242	AA	SEQ	243	AA	SEQ	244	AA	SEQ	245	AA	SEQ	246	AA	SEQ	247	AA	SEQ	248</
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Table 3 (cont'd)

Tissue	Tumor sym	Normal sym	Tumor to	Tumor cells	Normal	Endes	p31	SEQ 36 AA	SEQ 37	WYSEQ 44	AA SEQ 43	NE SEQ 66	CS SEQ 64	HR SEQ 110	RSEQ 73	HR SEQ 76	AA
CRL 1				166				865	4675	157	1028	972	159	1954	17285	29406	
CRL 2				168				531	975	227	978	27	889	204	8255	45518	
T47D				169				5005	8316	0	1074	352	569	2901	19222	39931	
Ken-3				171				0	1953	0	234	13	137	1787	135	37072	
CRL 1441 RNA B/30				181				276	3104	0	24	0	0	1050	0	13079	
T811 uncased + DPhase				183				197	1800	0	65	0	0	943	230	14563	
KB poly A				194				0	5094	0	108	0	149	1816	620	31810	
HQS poly A				196				297	3283	8277	0	0	578	2815	868	52778	
ACHN				196				0	8593	0	358	0	1158	4907	145927	26142	
UACC-62				200				1497	9993	0	212	0	275	2225	2625	17324	
WCE-TADARIES				202				185	2228	753	0	0	381	1444	2567	14603	
UTOS (Mundy) poly A				204				0	7612	0	104	0	0	1028	617	9607	
WISH (Collagen) poly A				206				150	0	0	94	189	833	579	225	11442	
5S rRNA mRNA				208				0	18176	0	633	53	0	2367	2915	60563	
COL13 RNA 32/08				218				219	1862	0	206	0	261	993	815	73044	
WAL30 72h 0.5%FBS, 24h 10% FBS				219				271	3187	1190	0	34	403	2293	0	41474	
CRL 1441 + TPA (24h) B/30				220				0	5582	0	31	633	0	1066	63	18180	
Ken-1				221				2780	2513	0	61	0	452	2919	158	45266	
Ken-2				223				705	2808	0	1154	0	302	2129	41	41271	
Ken-4				225				521	4049	0	31	0	1303	2242	85	36345	
HOP-97				241				0	2362	0	218	0	87	1773	13338	19084	
MOL T 4				242				646	6364	762	493	481	2628	3182	35419	23972	
ECV4				243				22	13083	0	328	73	2139	6462	109714	30253	
HL 60				244				0	14211	886	23	431	2407	3685	15992	39367	
NCH-H7				245				950	13057	572	2945	167	3423	5364	95598	46201	
RPW B226				246				0	1320	489	179	0	354	2272	18378	26669	
ASWATCC				246				85	3450	691	518	304	0	1921	2785	58914	
SR				248				0	1814	363	9	23	244	2897	16201	17282	
OVCAR-3				249				0	7307	0	214	120	1028	2424	7704	20878	
HCT-15				250				0	10785	599	1456	0	3538	4642	105630	27562	
OVCAR-4				251				223	294	1330	473	905	473	905	1481	7673	
UVC-31				252				372	3404	0	0	6	143	547	1109	6260	
OVCAR-5				253				2585	9438	1611	675	52	1734	3343	12208	24504	
SN12C				254				0	5117	504	176	108	3335	2875	26805	16317	
OVCAR-8				255				0	2508	868	213	0	1122	1359	35633	14140	
OS BFL				256				823	17296	4093	698	61	5003	5293	30147	36545	
HOROV1				257				1194	8352	758	716	68	2032	3644	28934	31704	
SK-MEL-2				258				0	5305	0	19	0	0	963	4987	15816	
SK-LV3				259				65	3527	0	200	0	1050	3782	8318	17004	
SK-MEL-5				260				195	3911	0	48	101	148	381	13542	31421	
SP-539				261				3532	12225	0	664	150	7673	5550	62279	51506	
SK-MEL-28				262				0	7037	0	384	0	1713	1591	5611	34907	
K-562				263				587	8200	1949	1685	29	9059	4576	195694	61739	
UACC-257				264				0	6275	0	408	150	2865	1436	29055	29055	
M14				265				0	2639	0	0	214	804	616	1176	17725	
MCF7				267				829	16845	820	965	604	4658	6019	79777	80630	
MDA-MB-435				269				144	6376	477	543	0	968	1657	1148	24187	
HT270				270				14	4483	0	0	0	931	5525	28	41301	
MDA-N				271				276	7065	0	354	92	1299	1838	5866	18906	
Y79 poly A				273				0	8894	0	379	0	3785	6025	24954	77861	
CHOS poly A				289				0	20758	17443	3711	236	6785	4275	36066	76981	
HTB36 24h TPA RNA B/3				290				783	3861	0	728	0	2298	1937	221	31817	
HELA EXP 031830				313				634	1812	0	247	0	1500	2048	4161	39714	
HTB36 On RNA				322				1461	24464	0	0	969	3512	8180	3044	81664	
HT347				323				404	5560	0	0	0	2939	3484	15622	48011	
5S rRNA RNA				324				1327	4573	0	68	748	990	4386	60606	60606	
HCL4226				336				677	6101	721	345	0	1515	7111	2329	37118	
HOP-62				337				0	15366	0	906	78	2808	1717	36496	21036	
MDA-MB-231				338				1085	85815	1217	5738	1717	25352	13718	258035	103178	
U251				339				132	80374	1171	18256	362	78784	33626	2025349	111922	
PT Cells poly A				340				483	1682	0	467	0	1987	2005	45862	16256	
PC-3				341				177	13879	62	362	2730	5703	6884	40554	71885	
HCC-2998				343				92	8206	0	552	369	1782	2280	23873	21576	
SW-620				345				29	1776	0	621	202	1201	2048	10733	24715	
HT192				347				1001	7250	408	182	0	1412	5254	2082	65023	
GCO-205				347				162	8047	0	305	0	0	685	1304	8915	
HT218				348				440	4819	0	72	158	0	1385	291	36488	
OS-12				348				49	11052	0	406	0	891	1119	34049	11488	
HT151				350				138	6054	0	0	0	723	3737	4871	45600	
A498				351				797	20305	0	401	1964	1038	2640	4743	30375	
HT300				352				726	15335	57	91	0	2022	4435	5637	60935	
EXP 393				353				0	8072	0	114	752	3481	7229	7229	7229	
TK-10				355				738	78660	694	1780	1673	23020	12524	129750	71952	
Melms-344				357				2111	93276	13897	36786	2444	55479	34972	201421	150800	
He S187				359				0	9184	0	88	82	2391	2875	6581	48992	
HT13	50			50				0	21407	417	918	1707	0	0	0	52671	
HT286	52			52				179	8067	0	0	272	783	2581	7541	84143	
HT139	54			54				921	8243	0	4	635	0	1926	276	65037	
HT155	56			56				0	6599	0	281	632	2354	2131	2121	61017	
HT163	58			58				1082	34	302	364	291	281	1598	540	61835	
HT170	60			60				37	15071	0	252	0	1662	4224	15427	83039	
HT172	62			62				0	3376	0	0	17	284	975	0	46245	
HT138	63			63				0	2673	0	0	43	767	1070	4034	45891	
HT176	64			64				31	31195	0	0	1415	349	974	606	61835	
HT154	65			65				0	1277	2364	0	44	108	1138	0	52719	
HT180	66			66				276	2597	0	58	0	862	865	197	43129	
HT169	67			67				427	4840	0	0	229	209	455	1239	26590	
HT180	68			68				69	4083	286	122	0	346	1043	3365	78481	
HT143	69			69				2067	248	0	0	161	828	42	38405		
HT190	70			70				0	5719	954	58	0	0	1854	0	59929	
HT145	71			71				1053	3301	539	0	74	3282	1633	230	56887	
HT227	72			72				0	8795	0	33	163	2496	1928	271	65548	
HT202	73			73				0	18128	0	439	112	0	2601	865	84661	
HT314	74			74				0	10943	138	0	41	279	1755	1196	51097	
HT317	76			76				275	25797	0	2002	651	86	5151	5403	100831	
He S187	77			77				0	3161	0	126	250	0	3011	615	39514	
HT229	78			78		</											

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Table 3 (cont'd)

	Tumor - y/m	Normal - y/m	Tumor - t/o	Tumor cells	Normal	Endose	p33	SEQ 34	AA SEQ 37	W3 SEQ 44	AA SEQ 43	ME SEQ 44	CA SEQ 45	HA SEQ 46	ME SEQ 110	RE SEQ 123	HA SEQ 124
HA-SZT	155							0	41445	647	1696	3447	2071	1561	6395	55674	
MCF-7ADR-RES	153							2256	18571	3302	2910	480	21332	2661	35921	54012	
MCF7	151							3968	30669	180	1920	2844	11886	3405	22510	81756	
M14	148							776	16782	0	704	437	6271	3690	4021	69404	
UACC-757	147							156	14876	1634	7208	163	6917	2193	17912	61726	
UACC-62	145							600	34105	0	2145	161	14531	1509	4231	41268	
SK-MEL-20	144							40	12032	4856	577	770	5176	10711	2990	56031	
UO-31	140							440	6859	1716	624	98	14005	2232	3034	10591	
SK-MEL-5	142							1182	27392	1994	1944	2909	13115	1215	5955	42911	
SK-MEL-5	141							325	5737	5512	104	5	1581	1311	64	48569	
SK-MEL-2	140							3267	14466	3221	795	1827	7349	1575	74791	62671	
NCI-15	138							140	12215	771	657	666	4927	2687	7421	71199	
HA-MEL-30	138							1725	25340	2545	2991	2553	10072	2036	7231	42561	
COLD-205	137							2484	34100	2795	0	1945	13401	1681	2407	96313	
LOA-BM1	136							303	37237	202	3101	4339	32433	892	8051	33724	
SW-620	135							630	6511	8	1807	1939	10151	1195	2766	26369	
TK-10	134							545	8477	1317	1506	9052	23808	1173	1178	42228	
HCT-116	133							1015	7388	0	148	413	1179	2013	14581	29595	
786-0	132							636	8319	827	1162	947	28069	1670	7153	41603	
MCC-2998	131							1700	9369	0	397	1115	8212	1984	3255	74996	
ACHN	130							610	8938	1426	1253	645	21377	1486	7923	49258	
PC-3	129							577	10321	0	33	809	14768	1450	3151	45570	
RDX-393	128							1067	12023	1588	4377	377	20806	1604	13035	43631	
DU-145	126							120	1048	100	126	178	4902	2174	3956	46330	
Cam-1	125							981	13976	561	2889	334	4696	1932	15837	42079	
SR	125							0	9755	0	1098	357	1724	2308	4070	44871	
A498	124							9313	19849	751	299	0	14129	2475	10609	49897	
RPMI-8226	123							0	5461	0	1	112	580	3030	5708	65175	
SM12C	122							0	173231	0	2502	134	6784	2447	106771	75897	
HS-60	121							353	4211	641	146	240	1254	20572	2980	55054	
MOLT-1	120							299	10544	6273	2442	877	12121	369	32836	49584	
QVCAR-3	119							1044	4812	2234	360	508	6276	1771	3529	56039	
NCI-562	118							2174	12961	1436	240	16403	143151	14061	21344	44925	
QVCAR-4	117							1463	31173	508	4934	691	4841	14507	7736	55652	
CCRF-CEM	115							553	6652	2368	1091	179	3448	1421	25044	42501	
QVCAR-3	115							1113	7238	0	668	634	10017	1247	49525	41075	
SP-539	114							0	6556	2682	5258	887	16786	6991	24991	53287	
HOP-62	113							200	304	304	1051	2776	8751	678	16094	47319	
SP-295	112							1371	14738	0	3749	2445	18206	1303	66694	51944	
AS59ATCC	111							1233	11509	0	2329	1054	18414	10920	81207	32566	
SP-760	110							235	10129	1848	3385	1263	17982	2094	15285	24296	
NCI-H460	109							1614	8620	2187	3741	1811	22919	2279	10968	53640	
U251	108							1091	11864	2328	5799	870	15224	1506	32438	40200	
NCI-H460	107							252	7303	127	539	25	20036	10620	1580	60299	
SNB-75	106							3683	13987	3336	3212	413	11090	2166	20663	68294	
NCI-H460	105							0	7540	1418	508	329	14963	2894	9129	52719	
SNB-19	104							922	19491	1502	2987	372	7863	2478	12455	103492	
NCI-H226	103							0	10957	871	440	462	5154	2756	87021	5718	
SK-OV-3	102							872	18352	1788	5673	716	1791	3129	30387	54491	
NCI-H226	101							672	10901	3057	795	665	3356	3272	7830	55878	
IGROV1	100							0	8455	808	3388	217	4065	2078	31162	42476	
EXVX-1	99							347	7233	697	574	5434	1940	4824	49958		
QVCAR-8	98							474	12037	2261	2837	792	13382	2385	31301	56630	
HOP-92	97							1566	4200	0	3536	215	24750	1814	5365	92500	
In Glioblastoma 3/31/92 #12	48							37	3414	0	477	601	26787	1456	10148	75029	
In adult SMC 10/2/92 #17	47							4753	10627	0	2520	7014	18804	1176	5151	72016	
In human melanocyte 2/25/92 #10	46							589	12403	551	39815	701	5629	2429	9414	61036	
TCAP	26							wt	0	2806	567	13218	0	1876	331	14896	19283
AS49-1								wt	0	3582	0	363	0	317	314	3847	10191
AS49-3								wt	0	2789	0	1896	0	623	157	11425	16623
AS49-4								wt	0	4433	0	2473	0	496	242	15445	13282
AS49-5								wt	0	3415	0	579	0	1983	281	12740	20201
AS49-7								mutant	0	7919	218	10495	0	2358	802	27454	14020
EXVX-1								mutant	0	6698	0	7440	0	2883	154	78154	19451
EXVX-4								mutant	0	4165	0	6533	0	1342	397	7118	16620
EXVX-3								mutant	0	2062	442	1504	0	2086	781	18082	27269
EXVX-5								mutant	0	3065	1404	40	0	1233	1305	5245	36616
EXVX-7								mutant	0	4366	0	3665	0	267	11222	15661	
MCF-7-1								wt	0	4324	0	2219	0	177	321	16876	14271
MCF-7-3								wt	0	2671	902	297	0	707	191	16894	15090
MCF-7-4								wt	0	4649	0	312	0	0	60	2437	14499
MCF-7-5								wt	0	2815	0	341	0	38134	118	9134	14350
MCF-7-7								wt	0	13125	0	4465	0	1135	950	48482	43329
ADR-RES-1								mutant	0	13125	0	4465	0	1135	950	48482	43329
ADR-RES-3								mutant	0	7895	206	1643	0	543	715	8378	15627
ADR-RES-4								mutant	0	1513	612	79	0	1047	335	10666	22094
ADR-RES-5								mutant	0	3674	0	5674	0	572	116	18216	11995
ADR-RES-6								mutant	0	50373	0	1519	0	635	310	4944	17965
ADR-RES-7								mutant	0	11054	0	1743	0	490	816	23088	21030
WI-38-1								wt	0	9568	317	2632	0	2774	717	23798	12714
WI-38-4								wt	0	8701	0	184	0	2780	796	25508	14200
WI-38-5								wt	0	8553	0	1867	0	1877	750	6930	17163
WI-38-7								wt	0	8181	461	897	0	866	1033	12862	13393
HeLa-1								HPV E6	0	2972	1045	125	0	763	361	8640	12311
HeLa-3								HPV E6	0	1915	299	2509	0	296	308	19037	12311
HeLa-4								HPV E6	0	1802	787	1330	0	283	119	11306	10796
HeLa-5								HPV E6	0	8774	343	2858	0	2129	634	36267	18512
HeLa-7								HPV E6	0	5057	0	1004	0	1673	860	16574	13815
HT-29-1								mutant	0	5732	0	1828	0	488	749	12309	13626
HT-29-3								mutant	0	7969	0	3638	0	581	547	14846	12452
HT-29-4								mutant	0	11578	0	3503	0	1997	567	32306	15923
HT-29-5								mutant	0	3290	0	2060	0	1547	552	2675	1784
HT-29-6								mutant	0	8747	67	2647	0	565	224	13578	13714
HT-29-7								wt	0	1778	0	2923	0	363	729	7747	14837
AS49-2								wt	0	4310	0	1755	0	896	366	16174	16569
EXVX-2								wt	0	802	0	1151	0	1867	1682	13242	6163
HT-118-1								wt</									

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Table 3 (cont'd)

Tissue	Tumor sym	Normal sym	Tumor - 1a	Tumor cells	Normal	Endos	p53	SEQ 56	AA	SEQ 57	WT	SEQ 60	AA	SEQ 63	NE	SEQ 66	CA	SEQ 68	HR	SEQ 118	B	SEQ 123	HR	SEQ 128	AA
DaFang-7								0	50728	3124	2203	0	2729	1021	16539	11948									
DaFang-8								0	35361	84	3207	0	2819	569	23616	14951									
DaFang-9								0	28319	0	4298	0	4297	174	52151	12734									
DaFang-11								0	40638	0	6023	0	3724	1086	49305	13175									
DaFang-12								0	16274	0	1652	0	2814	892	56983	11807									
DaFang-10								0	18015	0	1365	0	42701	801	34062	11401									
DaFang-1								0	11739	0	214431	0	20581	10521	20203	22794									
DaFang-2								0	9371	0	13705	0	1328	783	15252	16156									
DaFang-3								0	6905	1171	95151	0	503	923	31807	25569									
DaFang-4								0	4899	0	510	0	1746	690	20143	25155									
DaFang-5								0	3723	0	716	0	1018	948	9931	12544									
DaFang-6								0	39944	0	0	0	465	482	1929	9565									
AS49-8							wt	0	4018	537	1675	0	2260	398	19015	13833									
EXVX-8							mutant	0	6749	0	5081	0	4361	803	24268	14160									
HCT-116-7							wt	0	2945	597	89	0	812	478	8413	12883									
HCT-116-8							wt	0	5165	3418	899	0	591	391	11432	18508									
HT29-1							mutant	0	2474	0	1963	0	1494	451	29516	21737									
HT29-7							mutant	0	1053	0	54	0	307	209	9185	13162									
HT29-8							mutant	0	4333	0	2962	0	709	594	16207	19784									
SF539-7							wt	0	8603	0	866	0	1074	1086	12408	17808									
SF539-8							wt	0	8956	0	150	0	856	911	14376	16098									
SF-268-7							mutant	0	6810	1896	708	0	1316	420	14248	15443									
SF-268-8							mutant	0	9705	0	1884	0	2052	568	12101	14424									
OVCAR-4-7							wt	0	1789	0	507	0	591	100	3378	14756									
OVCAR-4-8							wt	0	8000	789	12121	0	3077	730	17308	16946									
OVCAR-5-7							mutant	0	6291	0	1758	0	18	1330	20088	37871									
OVCAR-5-8							mutant	0	3819	11046	46	0	2526	289	8074	10551									
MCF-7-8							wt	0	4047	348	1398	0	543	451	15957	16344									
ADR-RES-8							mutant	0	4033	485	2693	0	479	92	7975	12562									
HsLA-8							wt	0	4132	814	1078	0	1073	705	11463	19305									
SW480-7							mutant	0	3841	555	846	0	1028	212	13765	11456									
SW480-8							wt	0	3095	0	133	0	215	455	18823	10348									
HT29-8							mutant	0	8441	8724	1442	0	987	460	8507	12969									
C3A-7							mutant	0	6455	0	131	0	934	331	1068	11745									
C3A-8							mutant	0	4384	0	456	0	1860	1422	9025	25099									
UZOS-7							mutant	0	5403	395	0	0	1874	251	21545	16536									
UZOS-8							mutant	0	4223	1977	1921	0	2486	614	32458	11293									
HsLA-7							wt	0	4735	17844	462	0	888	614	10835	18314									
HsLA-8							wt	0	4538	0	1181	0	573	583	35697	17704									
WI 38-8							wt	0	8860	0	0	0	2756	690	1133	17515									
458 methyl RNA							wt	219	10478	0	4697	322	11543	2288	4332	123911									
CR15/2 3/17/89							wt	0	1475	79	288	0	0	1482	969	33847									
Bov-4							wt	1359	7178	0	471	66	4171	2041	13126	60734									
HT368							wt	115	10978	366	132	228	1211	1094	51273	96									
HT378							wt	334	1670	0	43	0	970	1344	481	84586									
HT385							wt	2684	23718	1052	187	825	1605	3482	3271	115925									
HT308							wt	494	4362	0	0	167	1896	2614	7469	23383									
Bov-3							wt	142	2903	68	0	0	1453	2663	25173	47964									
Bov-5							wt	175	1326	807	54	0	83	1943	678	27812									
Bov-9							wt	177	0	1932	516	109	0	315	1821	763	37803								
Bov-10							wt	1100	3331	611	85	0	878	1031	1884	280	44367								
HTB10							wt	1100	3331	611	85	0	878	1031	1884	280	44367								
h. ferrobacter 3/31/92 #12							wt	165	4732	0	30	9	1643	2487	1197	84103									
proline h							wt	97	709	66	151	47	840	1629	0	71260									
MHW-OS poly A+							wt	0	8770	1806	200	186	2527	2610	834	66336									
SA-OS (Mawyl) poly A+							wt	588	31225	0	101	1671	2913	2963	3973	62966									
MK poly A+							wt	272	28963	0	36	1131	4200	3944	5141	46333									
HCT-116-3							wt	0	2264	530	2001	0	506	457	6561	14135									
HCT-116-4							wt	0	3670	171	839	0	388	241	16248	13244									
HCT-116-5							wt	0	8838	209	724	0	477	389	13553	16473									
HCT-116-6							wt	0	5156	1378	2077	0	263	463	11650	12955									
AS49-6							wt	0	777	0	42	0	999	315	2191	14664									
HT29-3							mutant	3201	1117	2356	0	1884	311	14621	15623										
EXVX-6							mutant	0	919	80	0	0	367	636	9049	16148									
HT29-4							mutant	0	771	1454	875	0	899	409	13595	21158									
HT29-5							mutant	0	3498	1303	4091	0	1033	1063	25245	27154									
HT29-6							mutant	0	3158	171	2404	0	1130	1090	29241	30150									
OVCAR-4-3							wt	0	869	1624	4736	0	764	229	81071	12950									
OVCAR-4-4							wt	0	3487	0	1105	0	385	88	11844	11168									
OVCAR-4-5							wt	0	12920	1901	4206	0	807	375	86133	14195									
OVCAR-4-6							wt	0	3670	171	839	0	388	241	16248	13244									
SF539-3							wt	0	8954	177	706	0	920	168	8632	15284									
SF539-4							wt	0	11231	435	204	0	413	194	14686	10033									
SF539-5							wt	0	12548	396	469	0	642	352	4084	13377									
SF539-6							wt	0	5156	0	0	0	2221	267	14523	20184									
OVCAR-5-3							mutant	0	4326	296	1341	0	1507	482	8621	14804									
OVCAR-5-4							mutant	0	3508	0	1061	0	848	8731	13868										
OVCAR-5-5							mutant	0	2838	0	69	0	766	105											

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - to	Tumor - cals	Normal	Endo	p33	SEQ 79	AA	SEQ 80	SEQ 81	SEQ 82	SEQ 83	SEQ 84	SEQ 85	SEQ 86	SEQ 87	SEQ 88	SEQ 89	SEQ 90	SEQ 91	SEQ 92	SEQ 93	SEQ 94	SEQ 95
adipose gland - h	1							0	336	16727	26452	189725	3671	1988	818	261	12721								
adipose node - h	2							0	160	25283	33356	133215	10251	10251	818	261	12721								
bone marrow - h	3							0	407	9924	25669	90869	5274	447	0	19523									
breast gland - h	4							0	0	4132	3261	30513	30	24	1001	2064									
breast node - h	5							0	0	11466	9976	136456	8152	3520	611	12106									
breast node - h	6							0	530	9084	17023	100224	2051	1952	2411	11509									
breast node - h	7							0	336	18448	41689	94237	108261	4741	496	21132									
breast node - h	8							127	142	5620	82715	134453	5051	4401	29	11632									
breast node - h	9							171	354	10859	22941	102430	3445	812	55	23399									
breast node - h	10							717	1004	12254	187967	6384	358	201	10751										
breast node - h	11							256	639	28110	24184	87526	5311	903	224	14839									
breast node - h	12							511	83	11315	8647	222814	217	1878	74	11687									
breast node - h	13							436	207	10229	9496	116434	1904	430	266	8614									
breast node - h	14							0	532	13849	7790	102290	4593	2038	751	9415									
breast node - h	15							0	660	27774	19719	159648	6148	1076	177	13841									
breast node - h	16							191	1969	164918	11019	194752	19361	22613	26	3341									
breast node - h	17							266	1084	115085	85081	82687	2299	67611	0	4512									
breast node - h	18							220	255	25312	14108	103642	33951	12201	46	7578									
breast node - h	19							85	340	7756	11094	84387	7363	877	41	3903									
breast node - h	20							372	254	4036	13651	165877	1734	304	500	2607									
breast node - h	21							78	266	5062	14869	95360	2254	345	333	4083									
breast node - h	22							178	542	16836	13532	56915	2203	337	163	5791									
breast node - h	23							0	28	12942	12134	71122	1605	1227	0	3742									
breast node - h	24							0	373	21247	22843	183540	8954	855	882	20800									
breast node - h	25							177	456	21278	27103	112750	3463	790	290	30198									
breast node - h	26							0	128	5184	13178	104164	240	529	84	5251									
breast node - h	27							0	329	13848	8090	110349	7250	1464	322	10434									
breast node - h	28							122	0	0	4221	115750	11	378	7	6948									
breast node - h	29							0	438	15832	13708	86718	2751	1477	152	20177									
breast node - h	30							0	120	16146	8112	158944	1037	386	521	20177									
breast node - h	31							105	1371	61570	11725	94350	3629	1834	81	10397									
breast node - h	32							30	0	11102	3715	222698	260	320	0	6100									
breast node - h	33							0	130	20503	3248	127701	2284	1026	0	7444									
breast node - h	34							0	104	7145	484	17524	816	84	2563										
breast node - h	35							0	5	33026	1929	187218	302	513	0	3016									
breast node - h	36							436	37	6077	8883	65099	411	8	0	6065									
breast node - h	37							124	232	20525	4908	128875	699	23	333	4408									
breast node - h	38							362	0	2423	7235	15106	423	166	0	6253									
breast node - h	39							0	0	4472	83230	76	87	96	6253										
breast node - h	40							534	204	1307	15012	1837	1024	330	260	7758									
breast node - h	41							4	170	4203	8535	110729	1547	36	181	3289									
breast node - h	42							441	218	5677	17243	60667	33297	34	5251										
breast node - h	43							156	34	0	1327	1611	0	384	49	2573									
breast node - h	44							365	0	0	1256	0	0	300	82	563									
breast node - h	45							361	44	8	0	5096	0	238	16	87	304								
breast node - h	46							356	356	2541	0	4370	39918	47	1438	180	968								
breast node - h	47							354	354	4181	44	158	9008	36493	530	675	263	10146							
breast node - h	48							344	76	41	0	3634	0	419	60	0	2922								
breast node - h	49							342	255	156	230	2481	0	228	87	0	284								
breast node - h	50							334	260	0	0	15025	0	106	87	0	210								
breast node - h	51							332	15	0	0	15025	0	106	87	0	210								
breast node - h	52							332	0	0	501	8165	0	128	0	1881									
breast node - h	53							328	848	0	5021	26068	83113	442	888	447	7313								
breast node - h	54							327	98	0	212	26068	83113	442	888	447	7313								
breast node - h	55							326	2858	83	1171	11725	20188	196	671	0	5962								
breast node - h	56							321	0	20	0	2956	0	0	246	0	2392								
breast node - h	57							320	253	0	9489	8511	77832	1049	307	204	1080								
breast node - h	58							318	447	304	8168	17769	110877	10211	124	13291									
breast node - h	59							316	527	220	28285	6949	19058	2428	853	79	9214								
breast node - h	60							314	230	470	20940	12996	4852	10045	1002	273	14507								
breast node - h	61							311	90	52	42	7345	316	173	8	152	1743								
breast node - h	62							309	0	21	330	2837	0	145	49	0	1473								
breast node - h	63							307	258	8	5486	19	169	578	150	1445									
breast node - h	64							305	0	11	196	4777	8571	4351	58	0	2549								
breast node - h	65							303	146	756	3409	7475	7351	1902	150	341	5881								
breast node - h	66							302	558	2164	1446	18133	505	400	10	1963									
breast node - h	67							300	1134	7085	11747	7081	3876	2577	1281	15783									
breast node - h	68							298	248	344	14941	72841	123551	1178	1069	385	8920								
breast node - h	69							296	296	0	244	702	10569	466	2547	132	153								
breast node - h	70							294	456	43	518	6105	12699	6275	885	311	11686								
breast node - h	71							292	136	94	1930	4523	229	419	331	134	5512								
breast node - h	72							290	633	1809	36493	18470	6769	3133	1326	224	15796								
breast node - h	73							279	0	0	0	1133	0	16	0	168	1010								
breast node - h	74							277	0	0	852	1607	246	25	0	2444									
breast node - h	75							275	110	124	2787	172	0	0	731	1817									
breast node - h	76							273	215	275	0	1285	0	115	82										

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Table 3 (cont'd)

Tissue	Tumor sym	Normal sym	Tumor - to	Tumor cells	Normal	Endox	p53	SEQ 78 AA	SEQ 802a	SEQ 82 MU	SEQ 84 RIF	SEQ 88 AA	SEQ 89 AA	SEQ 90 M	SEQ 93 TS	SEQ 94 AA
C-Mu-1			166					279	236	10781	1332	0	782	0	0	1369
T-602			165					132	83	9630	4542	3003	4163	130	0	3588
T-47D			169					0	235	19539	3970	63	2558	414	0	11668
Kan-3			171					49	0	0	1622	6713	0	61	0	2573
CR1441 RNA 6/30			181					0	244	0	0	1791	0	1	126	543
T811 untreated - O/Vacc			183					0	0	0	321	111	0	0	0	264
KB poly A+			194					114	6	541	2325	0	50	1	0	3703
HOS poly A+			196					218	0	1363	3269	0	0	101	190	3424
ACR10			198					0	122	10672	1171	549	147	150	63	1871
UACC-62			200					165	0	3877	0	2173	244	0	163	4052
WCF-7ADR RES			202					100	0	1497	402	215	148	0	0	2877
UTOS (Murex) poly A+			204					112	0	0	330	0	79	252	124	498
WISH (Collagen) poly A+			206					0	209	613	637	315	8	0	0	1576
ESM melanoma mRHA			208					1183	0	2134	2543	826	880	0	167	8071
CC-137 RNA 3/21/80			218					0	0	292	1884	0	25	143	6	2126
W136 72h 0.5%FBS 24h 10% FBS			219					0	0	101	3363	416	635	194	0	3255
CR1441 + TPA (24h) 8/30			220					0	154	0	177	0	0	5	71	1123
Kan-1			221					0	55	0	0	0	0	0	0	2555
Kan-2			223					95	0	45	1182	144	0	133	0	2250
Kan-4			225					0	239	0	622	0	11	24	0	1278
HOP-82			241					0	0	1788	1888	963	185	216	0	2935
MOLT-4			242					85	163	8463	1928	2895	153	160	48	5219
BOYA			243					0	0	22076	1594	968	311	2045	0	5045
Hs-60			244					0	226	14060	2051	0	44	215	0	4254
NCH403			245					0	1087	77132	1403	0	700	225	5	5646
RPMI 8226			246					0	0	0	611	928	57	0	0	2
ASWATCC			247					0	0	4447	2653	0	168	164	0	2544
SR			248					0	163	10413	855	1682	589	17	0	2103
OVCAR-3			249					0	148	5905	1324	168	0	60	218	4524
HCT-15			250					129	0	45266	1486	291	569	0	55	5023
OVCAR-4			251					113	0	2861	54	0	169	0	167	1032
UO-31			252					209	0	307	480	0	36	0	151	1421
OVCAR-5			253					0	80	577	3409	0	1472	8	0	4319
SN1GC			254					496	0	6396	173	0	0	322	192	4185
OVCAR-8			255					181	0	17458	495	0	58	129	0	1761
LOX BAY			256					0	2638	92675	1953	3515	1363	0	154	5249
IGROV1			257					140	73	32974	1309	565	126	0	326	4424
SK-MEL-2			258					0	167	4482	224	1854	0	48	567	1286
SK-OV-3			259					0	19	4361	113	1949	581	0	71	1009
SK-MEL-5			260					0	101	3676	172	0	26	0	41	1617
SP-539			261					159	0	73632	1693	2508	925	496	174	4144
SK-MEL-28			262					187	0	14342	1446	0	0	86	0	1275
K-562			263					0	118	39031	825	1518	433	74	0	2890
UACC-257			264					0	83	6659	1900	873	91	109	0	1237
M14			265					0	21	1255	873	3737	0	121	0	2709
MC77			267					126	256	23780	5286	7090	0	715	0	14882
MDA-MB-435			269					0	0	9781	863	0	147	290	126	4006
HT279			270					38	26	0	1064	0	67	170	29	3572
MDA-N			271					0	0	14738	415	0	441	336	0	4126
Y79 poly A+			273					11	3611	6694	4474	0	1320	0	345	17179
K403 poly A+			289					25	3623	15982	6570	1854	2133	1051	0	21810
HTB36 24h TPA RNA 6/23			300					71	0	0	6206	0	0	40	153	756
HELA-EXP 0318/99			313					37	52	0	4774	0	9	153	97	3084
HTB36 on RNA			322					344	0	618	6852	16718	0	650	0	4427
HT347			323					0	59	4289	210	377	462	0	452	5452
#58 melanoma RNA			324					942	14	0	8157	8597	491	556	170	1553
NCH4026			336					262	21	11463	1217	1515	0	171	0	0
HOP-82			337					0	0	10627	2335	0	236	139	0	3071
MDA-MB-231			338					813	1127	121898	15066	39122	9266	1667	45	13415
U251			339					486	1740	724467	8096	60552	28673	1514	0	19652
PI cells poly A+			340					0	112	8025	709	0	445	128	27	2066
PC-3			341					513	215	25375	1044	18117	1417	1087	0	5652
HCC-2998			343					0	3	7505	1212	704	179	529	0	3025
SW-620			345					69	6	23824	1150	1491	32	243	0	2487
HT182			346					46	0	1580	8307	0	15	245	0	8569
COLO 205			347					17	60	3655	846	634	0	481	0	8140
HT214			348					0	1	612	5285	0	22	0	0	2261
KM-12			349					0	81	8666	3506	913	0	158	0	1180
HT151			350					32	202	352	7122	0	152	305	22	6687
AA98			351					537	11	6123	3776	2335	0	388	0	2292
HT383			352					235	0	14919	186	0	183	0	0	3522
RX2-383			353					350	0	8025	2120	3003	152	219	0	1907
TK-16			355					2370	1831	54066	4635	36193	4080	568	173	6202
Melan-34			357					1422	1373	162139	14530	51277	9889	967	88	6356
Pa-S187			359					164	43	21188	1289	1167	1033	150	12	4328
HT213		50						0	0	707	2103	0	660	336	0	14318
HT288		52						146	0	647	3338	0	69	594	0	19288
HT139		54						174	0	0	2792	0	59	307	27	5594
HT155		56						0	13	2563	0	0	80	0	0	15806
HT163		58						375	0	118	1588	0	412	161	117	8436
HT170		60						713	0	2417	1494	1868	0	719	0	13133
HT172		62						111	8	95	2349	0	0	29	0	6924
HT158		63						384	24	0	3179	0	0	0	0	5439
HT178		64						0	78	147	3414	0	821	40	0	6823
HT154		65						208	0	374	2620	0	0	607	0	12319
HT180		66						43	122	437	3609	0	0	0	45	3531
HT169		67						0	118	0	1861	0	0	340	182	2959
HT189		68						43	838	2833	3650	0	664	93	78	6023
HT143		69						327	0	0	2961	0	0	167	0	632
HT180		70						362	71	1366	6366	0	209	268	0	1551
HT145		71						84	68	2884	4726	0	0	230	0	828
HT227		72						12	0	215	3473	0	1015	464	0	2504
HT302		73						143	0	2618	7386	1850	4134	721	174	25415
HT314		74						230	0	674	3847	0	836	349	0	11481
HT317		76						285	81	345	7369	706	979	805	238	13106
Melanoblastoma 8425 11/8		77						0	0	9	2662	0	0	68	0	87
HT323		78						0	0	5081	4645	0	297	198	0	8445
HT327		80						0	83	230	1542	1133	0	16	45	2807
HT335		82						0	0	0	4194	8	258	0	0	8152
HT146		85						48	5	831	0	0	38	0	182	1384
HT348		87						69	156	150	5529	0	1017	0	0	3424
HT311		170						238	0	0	3176	0	130	5	111	5105
HT308		185						673	0	0	1176	1616	0	382	0	6621
HT140		187						230	117	0	0	0	188	359	0	546
HT281		189						303	0	0	1					

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Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor - to	Tumor cells	normal	Endo	p53	SEQ 79 A	SEQ 82 A	SEQ 82 B	SEQ 84 A	SEQ 84 B	SEQ 88 A	SEQ 89 A	SEQ 90 A	SEQ 93 A	SEQ 94 A
HA 5721	155							275	156	133245	4602	2616031	30771	326	831	3393	
MCF7ADNR-RES	153							454	0	62589	3763	173587	840	234	71	4602	
MCF7	151							0	96	22491	3843	219251	40	463	501	4546	
M14	149							34	0	102635	5786	68636	134	4631	181	8105	
UACC-257	147							0	190	44964	4456	46556	1177	1771	77	5052	
UACC-258	145							0	331	105560	8515	47918	1123	348	0	8145	
SK-MEL-2	144							0	103	35141	6515	65339	515	133	24	1592	
UO-31	143							508	100	20649	9249	73214	320	189	275	1529	
SK-MEL-5	141							104	0	29587	6756	73271	1055	79	111	2500	
WM-12	140							416	0	3454	3354	80653	109	127	182	3169	
SK-MEL-2	139							171	0	22619	3246	134929	27	187	132	2782	
HCT-15	137							0	47	15099	3913	104930	599	0	1031	7894	
Melan-34	136							148	150	22468	5765	137583	977	279	0	3750	
COLO 205	135							0	213	21011	5643	144441	642	91	74	5493	
LOX IMV	134							156	1464	58997	3350	112245	1470	0	0	3197	
SW 620	133							165	0	11595	3617	104947	788	0	210	6215	
TK-10	132							0	137	23867	4146	75724	1969	130	0	4536	
HCT 116	131							1020	59	74651	2016	119724	702	83	263	7449	
T86-0	130							225	0	26315	3039	102477	3314	0	42	6256	
HCC-T200	129							0	190	17067	5568	127191	455	16	0	3023	
AGHN	128							0	138	35733	4255	87608	473	165	144	2352	
PC-3	127							160	104	8373	2715	80475	1017	248	0	7409	
DU-145	126							134	204	75480	3502	59953	377	258	65	7546	
Caki-1	125							0	79	6334	2431	17433	259	54	0	2817	
SR	124							0	141	82167	2648	84362	3136	0	0	5203	
A438	123							0	79	8485	2504	28629	1849	80	47	10019	
PRM 8226	122							0	153	26455	2600	91356	15	1182	0	6392	
SM12C	121							24	0	80	2614	12634	103	473	156	4176	
HL 60	120							0	0	35753	7382	36641	542	512	84	11656	
MOL T-4	119							613	109	925	8301	450	369	314	173	21430	
OVCA-5	118							0	0	909	5372	83742	4346	27	0	3065	
K-562	117							425	0	620	4872	41219	4813	8262	171	1433	
OVCA-3	116							258	0	10918	4097	106477	228	97	70	6579	
CCRF-CEM	115							654	246	21540	2514	133148	8057	231	0	3791	
OVCA-4	114							0	0	16299	3482	113784	6977	144	0	5740	
SK-MEL-2	113							464	37	13067	2665	95833	1345	33	0	3461	
SK-MEL-2	112							217	0	14169	3682	95278	2383	119	0	5506	
SK-MEL-2	111							404	153	36836	1330	72109	2689	0	0	5448	
SK-MEL-2	110							281	6	21130	3579	98198	3313	0	5	13804	
SK-MEL-2	109							1005	321	44866	4014	130106	3058	220	0	4485	
SK-MEL-2	108							364	213	33068	7465	81136	3557	225	113	4126	
SK-MEL-2	107							292	0	24593	5009	148017	1964	183	253	7311	
SK-MEL-2	106							170	216	27031	2639	46575	3614	27	0	4205	
SK-MEL-2	105							166	335	5661	1862	68912	3641	143	0	8291	
SK-MEL-2	104							212	0	23147	4126	72618	1194	0	0	5616	
SK-MEL-2	103							139	58	6406	2982	17270	1903	0	87	6176	
SK-MEL-2	102							211	119	21514	5630	11321	4083	0	298	10600	
SK-MEL-2	101							0	0	5634	7381	18430	5044	212	171	3861	
SK-MEL-2	100							319	432	61716	2994	2378	1016	187	64	3911	
SK-MEL-2	99							0	282	6156	2107	15131	1772	413	215	12724	
SK-MEL-2	98							62	132	28182	4584	5729	813	312	0	1422	
SK-MEL-2	97							106	73	51373	5395	2665	2072	116	0	8109	
SK-MEL-2	96							0	254	18097	7191	3604	15079	305	0	12100	
SK-MEL-2	95							315	260	22446	6764	150645	4899	414	0	4885	
SK-MEL-2	94							0	0	1880	7249	127385	634	456	284	4382	
SK-MEL-2	93							0	0	13009	9192	188015	116	117	0	5760	
SK-MEL-2	92							0	16	11006	6235	81465	341	226	0	14132	
SK-MEL-2	91							0	49	3553	63185	0	3072	0	48	110	
SK-MEL-2	90							0	22	0	46138	0	0	0	276	598	
SK-MEL-2	89							0	62	118	46247	0	1843	0	342	754	
SK-MEL-2	88							0	306	2509	72567	0	2142	0	0	1102	
SK-MEL-2	87							0	58	631	39860	0	989	0	0	1377	
SK-MEL-2	86							0	296	2606	66834	0	4755	0	135	130	
SK-MEL-2	85							0	323	714	150881	0	10601	0	126	1699	
SK-MEL-2	84							0	359	49	77798	0	6784	0	0	824	
SK-MEL-2	83							0	16	1208	37631	0	898	0	187	2202	
SK-MEL-2	82							0	1153	80	74369	0	703	0	0	4666	
SK-MEL-2	81							0	550	0	41681	0	322	0	0	1185	
SK-MEL-2	80							0	234	0	37645	0	0	0	124	574	
SK-MEL-2	79							0	182	1025	32082	0	648	0	91	561	
SK-MEL-2	78							0	0	0	25975	0	880	0	429	1630	
SK-MEL-2	77							0	264	20	21865	0	0	0	0	697	
SK-MEL-2	76							0	744	1610	89435	0	2747	0	912	1775	
SK-MEL-2	75							0	911	2497	43852	0	860	0	175	1127	
SK-MEL-2	74							0	445	218	40537	0	1142	0	7	1422	
SK-MEL-2	73							0	0	30547	0	1779	0	231	248	0	
SK-MEL-2	72							0	473	4304	27945	0	1085	0	0	924	
SK-MEL-2	71							0	953	3084	67921	0	19059	0	110	2042	
SK-MEL-2	70							0	362	1018	45671	0	10256	0	0	308	
SK-MEL-2	69							0	0	1422	44081	0	8336	0	0	1232	
SK-MEL-2	68							0	16	1554	48543	0	7404	0	0	1057	
SK-MEL-2	67							0	27	365	32973	0	10729	0	189	1050	
SK-MEL-2	66							0	267	0	38078	0	997	0	140	1118	
SK-MEL-2	65							0	143	1244	43790	0	756	0	0	842	
SK-MEL-2	64							0	60	3030	41446	0	803	0	0	623	
SK-MEL-2	63							0	148	864	73772	0	1303	0	0	579	
SK-MEL-2	62							0	0	145	49694	0	856	0	151	1153	
SK-MEL-2	61							0	657	236	22779	0	1025	0	0	358	
SK-MEL-2	60							0	1745	1079	28134	0	4889	0	0	441	
SK-MEL-2	59							0	3584	1879	35500	0	14641	0	54	1027	
SK-MEL-2	58							0	80	15450	0	6835	0	0	0	1529	
SK-MEL-2	57							0	513	4627	23696	0	1177	0	115	577	
SK-MEL-2	56							0	0	2762	39578	0	1166	0	0	511	
SK-MEL-2	55							0	1047	85	73357	0	8236	0	60	1408	
SK-MEL-2	54							0	1062	308	62248	0	1884	0	0	1781	
SK-MEL-2	53							0	17	54	122573	0	7688	0	0	1283	
SK-MEL-2	52							0	148	556	341950	0	121	0	170	877	
SK-MEL-2	51							0	0	830	22567	0	2652	0	0	488	
SK-MEL-2	50							0	182	21	25248	0	4826	0	0	731	
SK-MEL-2	49							0	0	3696	43016	0	3529	0	436	1744	
SK-MEL-2	48							0	253	1236	85684	0	6089	0	170	303	
SK-MEL-2	47							0	1449	220	42305	0	7116	0	220	1914</	

Issue	Tumor type	Normal type	Tumor site	Tumor cells	Normal	Endos	p13	SEQ 79 AA	SEQ 80A	SEQ 81	SEQ 82	SEQ 83	SEQ 84	SEQ 85	SEQ 86	SEQ 87	SEQ 88	SEQ 89	SEQ 90	SEQ 91	SEQ 92	SEQ 93	SEQ 94	SEQ 95
Diapeng-1							0	1167	2281	84061	0	7232	0	238	15	428	720							
Diapeng-8							0	2758	63	72626	0	8513	0	48	103	670								
Diapeng-9							0	2323	15	36655	0	1281	0	10	103	720								
Diapeng-11							0	1	2518	73541	0	8194	0	1249	0	1179								
Diapeng-12							0	0	1603	47835	0	7669	0	0	0	1179								
Diapeng-10							0	34	0	33603	0	10777	0	0	0	515								
Diapeng-1							0	257	704	80021	0	2318	0	56	300	621								
Diapeng-2							0	408	295	146348	0	1211	0	31	45	303								
Diapeng-3							0	213	6567	106846	0	2713	0	0	0	584								
Diapeng-4							0	52	561	68193	0	559	0	354	601									
Diapeng-5							0	2555	0	45709	0	0	0	249	623									
Diapeng-6							0	1846	0	54509	0	56	0	10	492									
AS49-8							wt	0	28	4742	66151	0	2099	0	545									
ERVA-8							mutant	0	164	4621	74530	0	7705	0	0	2322								
HCT-116-7							wt	0	172	636	22256	0	1578	0	72	1568								
HCT-116-8							wt	0	205	779	28245	0	2302	0	176									
HT29-1							mutant	0	167	1301	47637	0	2716	0	215	852								
HT29-7							mutant	0	0	80	14674	0	90	0	95	441								
HT29-8							mutant	0	45	643	38186	0	342	0	0	459								
SF539-7							wt	0	254	114	26009	0	1532	0	124	813								
SF539-8							wt	0	100	116	38166	0	4181	0	0	1853								
SF-26A							mutant	0	0	2013	52411	0	2540	0	167	1480								
SF-26A-8							wt	0	1365	1825	39782	0	4138	0	126	1371								
OVCAR-4-7							wt	0	169	0	24881	0	534	0	140	2424								
OVCAR-4-8							wt	0	0	2400	56208	0	6788	0	0									
OVCAR-5-7							mutant	0	1141	660	98690	0	2132	0	0	3745								
OVCAR-5-8							mutant	0	791	476	13621	0												

[illegible]

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - fo	Tumor cells	Normal	Endo	p53	SEQ 95	AA	SEQ 96	AA	SEQ 97	AA	SEQ 98	AA	SEQ 99	AA	SEQ 100	AA	SEQ 101	AA	SEQ 102	AA	SEQ 103	AA	SEQ 104	AA
C638				166				229	226	308	131	1115	713	82	303												
T660				166				0	152	14	104	5501	1079	0	766												
L470				171				0	3	150	65	0	338	0	530												
Ker-3				181				31	447	0	1	81	747	0	526												
CR11441 RNA 8/30				183				0	203	0	0	173	64	236	0	396											
7811 untreated + DMSO				194				0	0	283	279	1030	237	0	448												
KB poly A+				196				0	0	131	139	163	260	0	474												
HOS poly A+				196				118	293	0	87	1048	685	0	553												
ACHN				200				227	691	0	64	1808	1271	161	408												
UACC-62				202				0	76	137	0	167	136	172	257												
MCF-7ADRI-RES				204				305	524	946	0	73	3428	156	431												
UTOS (Mundy) poly A+				206				0	0	808	0	293	474	0	197												
WISH (Colony) poly A+				208				712	1711	0	351	309	1345	0	758												
458 modulo mRNA				218				247	151	680	27	168	0	452													
CCL137 RNA 3/21/80				219				0	186	0	111	30	115	0	305												
W136 72h 0.5%FBS 24h 10%FBS				220				0	0	92	136	41	322	0	477												
CR11441 + TPA (24h) 8/30				221				0	80	0	9	42	212	164	577												
Ker-1				223				0	140	161	117	1001	117	0	478												
Ker-2				225				0	172	205	31	0	86	0	467												
Ker-4				241				0	0	197	155	365	80	0	66												
HOP-82				242				0	0	173	504	2918	787	524	294												
HOP-T-4				243				862	302	19	274	720	278	870	0	1896											
ECVx				244				2406	529	0	272	5737	330	65	18												
Hs-60				245				27	233	624	424	2576	193	0	337												
NCL403				246				0	450	847	146	1672	0	0	460												
HPM1-826				247				225	106	0	312	837	249	0	548												
A549ATCC				248				0	122	0	229	298	923	0	425												
SR				249				0	0	1127	321	3870	467	215	306												
OVCAR-3				250				18	423	54	448	1543	531	362	484												
HGC-T8				251				0	84	423	29	483	453	0	186												
OVCAR-4				252				197	270	0	207	62	34	0	41												
UO-31				253				0	816	0	73	8728	1339	0	351												
OVCAR-5				254				690	366	992	0	1416	396	452	597												
SN12C				255				753	0	0	19	153	245	0	276												
OVCAR-6				256				227	541	454	732	3166	614	357	703												
LOX IMVI				257				0	660	554	454	1607	399	189	626												
HQROV1				258				0	212	0	63	47	346	0	204												
SK-MEL-2				259				0	572	0	0	634	448	415	653												
SK-CV-3				260				211	0	0	0	1528	325	0	453												
SK-MEL-5				261				0	352	0	156	2049	1651	0	1121												
SF-538				262				0	894	1839	0	1332	1027	0	837												
SK-MEL-28				263				87	0	792	267	473	91	32	544												
K-562				264				0	0	70	2198	505	0	493	0												
UACC-257				265				406	0	0	70	414	119	114	186												
M14				267				472	0	0	2572	17839	1425	0	1304												
MCF-7				268				0	73	0	138	1633	109	0	36												
MDA-MB-435				270				0	626	0	41	0	1095	0	800												
MT-279				271				76	276	0	0	1375	488	647	221												
MDA-N				273				0	810	527	318	1534	1167	0	1461												
V79 poly A+				289				0	158	187	171	233	1831	0	513												
KHOS poly A+				300				0	363	85	216	37	0	0	404												
HT B36 24h TPA RNA 6/23				313				0	0	207	141	0	0	0	209												
HELA-EXP-031899				322				605	1211	0	129	225	1206	0	1175												
HT134 6h RNA				323				0	245	0	327	211	117	0	306												
458 modulo RNA				336				359	1654	0	0	58	1282	0	901												
NCI-M226				337				0	77	0	0	3462	464	0	514												
HOP-82				338				663	0	0	219	657	413	360	0	16											
MDA-MB-231				339				2821	1673	53	3315	26597	11907	1155	1018												
U251				340				136	0	0	292	659	229	26	144												
PT cells poly A+				341				362	1320	0	642	3095	1672	0	1051												
PC-3				343				300	845	283	44	1152	483	0	855												
HGC-2098				345				307	1338	0	20	1534	792	0	473												
SW-620				346				0	232	109	0	217	0	7	80												
MT-192				347				0	845	0	169	827	87	115	396												
COLO 205				348				0	309	41	0	0	212	0	446												
HT-118				349				0	1263	0	56	980	377	150	181												
KM-12				350				0	476	0	0	42	0	932	725												
HT-151				351				453	2054	628	277	273	587	299	572												
A498				352				10793	0	491	163	4354	54	700	0	455											
HT-293				353				173	1830	0	96	446	195	279	638												
RJF 303				355				4314	2783	0	658	3339	4922	402	1376												
TK-10				357				1135	4390	0	1484	27112	4961	1635	1624												
Mammary-3M				359				0	454	0	327	205	1421	545	354												
Ms 5781				50				0	951	949	257	17	1399	0	249												
HT-213				52				0	502	0	0	2784	1622	190	435												
HT-288				54				0	648	130	37	0	355	0	354												
HT-339				56				0	260	0	357	752	0	825													
HT-155				58				0	209																		

Table 3 (cont'd)

Tissue	Turner - ym	Normal - ym	Turner - fa	Turner - ca	Normal	Endo	p53	SEQ 83	AASG 96	AASG 97	HSEG 100	ARCO 981	ARCO 118	ARCO 111	ARCO 117	ARCO 114
Hs 52AT	145							2921	943	0	1780	2068	12004	10483	6651	14782
HsF-TADP-RES	151							4911	517	1977	891	696	10678	6354	892	0
MCF1	151							5433	1235	160	6856	3063	25634	2094	1309	2238
MH1	149							3831	0	450	2401	1993	2416	1359	1035	0
UACC-257	147							4027	268	1768	2776	2137	11053	6220	678	947
UACC-82	145							2545	157	726	756	1215	4403	2480	585	429
SK-MEL-28	144							5634	60	3906	1173	721	3098	1531	805	2594
UO-31	143							5324	487	3107	504	442	4000	1028	1536	11991
SK-MEL-5	141							1336	1059	2761	2926	16384	2964	807	1384	1366
KM-12	142							261	319	0	469	0	3403	379	443	0
SK-MEL-2	140							2614	185	1844	1741	479	19972	1171	918	3611
MCT-15	139							4802	486	655	1930	369	8956	682	978	1620
Mamma-3M	138							1296	40	563	2381	1143	2370	234	943	2899
QSO 205	137							1538	181	1093	1664	1417	11150	211	1214	1103
LDR-BR1	136							3524	52	1973	1526	677	23802	2457	267	1995
SW-620	135							4591	493	1395	1150	826	12216	571	650	1166
TK-10	134							4648	518	1681	895	494	9644	2857	821	1034
MCT-116	133							1224	344	579	1524	333	6640	3552	768	0
TBC-0	132							2784	163	1883	628	7921	11840	2318	722	0
HCC-2998	131							2684	29	0	1232	719	5639	858	904	0
ACHN	130							2287	486	2068	1970	936	360093	2458	6571	0
PC-3	129							5813	370	0	718	646	13046	2799	542	0
RCP 303	128							614	317	6314	911	540	2671	7592	524	105
DLL-145	127							1412	83	621	506	461	3331	1531	666	312
CWR1	126							21831	41	0	1328	635	64095	3476	502	1596
SRA	125							34171	320	841	0	841	19031	1183	345	84
A458	124							5481	0	1125	1967	269	26334	10429	628	1032
RPMI 8226	123							1951	46	44	226	354	1926	0	563	854
SN12C	122							2050	194	800	178	1633	11740	11038	637	637
HL-60	121							930	0	0	547	2164	395	636	0	0
MOLT-4	120							5683	0	1010	522	1507	4271	753	1205	0
OVCAR-5	119							1500	119	1759	1666	2515	8853	1900	925	5625
K-562	118							3787	0	0	850	252	6345	1008	1008	269
OVCAR-4	117							1258	26	0	1029	2229	11190	5861	1253	62
COIP-CEM	116							6623	86	1599	2572	1626	25632	2316	981	1348
OVCAR-3	115							2050	150	1633	934	1582	12158	1242	552	0
SF-539	114							3527	457	10	717	367	16926	893	68	1469
HOP-62	113							455	40	1559	673	265	19246	3406	781	1027
SF-295	112							2817	539	73	1118	801	17954	1580	941	0
ASBPATCC	111							1680	940	1723	2304	1701	30278	3221	1074	751
SF-268	110							2259	208	1443	583	814	11939	4209	630	1666
NCIH522	109							1264	1264	8	11167	1721	1721	1466	916	1741
UAB1	108							2200	209	729	977	733	8651	3516	520	2250
NCI-HM60	107							2274	449	1277	926	936	17629	1892	6761	0
SNA-75	106							1146	220	0	405	289	4322	1354	723	1
NCI-H322M	105							3365	435	0	3525	1047	2044	336	527	327
SNA-19	104							2096	316	0	1663	455	4358	2106	812	1908
NCI-H295	103							6463	125	0	1140	759	4785	1552	1091	0
SK-OV-3	102							6105	418	0	1085	615	12274	5271	587	3218
NCI-H23	101							6603	311	0	1163	841	7912	4463	386	0
KIROV1	100							0	212	0	1683	959	10757	0	493	0
EVX1	99							1881	170	77	1733	915	10990	1357	340	842
OVCAR-6	98							3654	0	477	422	150	7066	376	762	0
HOP-92	97							2307	158	0	698	628	13230	5619	881	0
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Tissue	Tumor - aym	Normal - aym	Tumor - to	Tumor cells	Normal	Endos	p31	SEQ 95	AA	SEQ 96	AA	SEQ 97	HES60	108	AGE0	101	AGE0	110	AGE0	111	AGE0	112	AGE0	114	M
DafPang-2								0	0	0	0	4153	258	0	1186	760	0								
DafPang-8								0	0	0	0	0	72	0	1336	364	0								
DafPang-9								0	0	0	0	352	17	0	2407	603	0								
DafPang-11								0	0	0	0	2910	477	0	1191	735	0								
DafPang-12								0	0	0	0	50	0	0	5103	384	0								
DafPang-10								0	0	0	0	11437	102	0	910	582	0								
DafPang-1								0	0	0	0	0	80	0	120	636	0								
DafPang-2								0	0	0	0	262	0	0	208	737	0								
DafPang-3								0	0	0	0	5099	69	0	1377	519	0								
DafPang-4								0	0	0	0	3575	67	0	3508	764	0								
DafPang-5								0	0	0	0	217	32	0	1090	645	0								
DafPang-6								0	0	0	0	0	0	0	62	1967	0								
AS49 - 8								wt				1852	49	0	59	622	0								
ESV1 - 8								mutant				6458	207	0	324	847	0								
HCT-116 - 7								wt				0	0	0	209	54	0								
HCT-116 - 8								wt				0	0	0	0	176	675	0							
HT29 - 1								mutant				0	0	0	3501	0	0								
HT29 - 2								mutant				0	0	0	3147	20	0								
HT29 - 8								mutant				0	0	0	467	0	0								
SFS39 - 7								wt				0	0	0	375	55	0								
SFS39 - 8								wt				0	0	0	0	252	0								
SF-260-7								mutant				0	0	0	446	164	0								
SF-260-8								mutant				0	0	0	0	183	0								
OVCAR4 - 7								wt				0	0	0	1305	423	0								
OVCAR4 - 8								wt				0	0	0	527	329	0								
OVCAR5 - 7								mutant				0	0	0	326	0	0								
OVCAR5 - 8								mutant				0	0	0	3115	558	0								
HCT-7 - 8								wt				0	0	0	740	194	0								
ADR-RES																									

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 Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - fm	Tumor - cfm	Normal	Endo	p53	SE0 116	SE
adrenal gland - h		1							94
lymph node - h		2							834
ovary - h		3							922
testis - h		4							0
uterus - h		5							2601
brain - h		6							235
coracohum - h		7							680
pancreas - h		8							2227
total brain - h		9							2719
placenta - h		10							1303
total kidney - h		11							717
prostate - h		12							702
total liver - h		13							537
adipose - h		14							548
total lung - h		15							410
skeletal muscle - h		16							0
heart - h		17							154
small intestine - h		18							514
kidney - h		19							292
apical cord - h		20							250
liver - h		21							51
Spleen - h		22							167
lung - h		23							456
stomach - h		24							894
testis - h		25							60
thyroid - h		26				26			332
HPAEC		29							0
HPTEC		30				30			168
breast - h		31							3128
HPAEC		32							91
uterus - h		33							196
HCAEC		34							160
pancreas - h		35							0
lymph node - h		36							170
skeletal muscle - h		37							71
total liver - h		38							1036
heart - h		39							102
thyroid - h		40							145
Quadriceps - h		41							123
Fetal brain - h		42							537
Subcutaneous - h		43							140
testis - h		44							0
HT218-normal					365				0
HT218-normal					363				0
HT157-normal					361				0
Base-13					356	356			1292
Base-12					354	354			1237
coracohum - h					344				85
organ - h					342				0
HPTEC					334	334			0
lymph node - h					332				139
h adult SAMC 10/21/92 #17					330				141
Fetal brain - h					328				70
HT208-normal					327				69
thyroid - h					326				396
HT143 - normal					321				0
HEPM 3d untreated					320				0
uterus - h					318				148
breast - h					316				203
thyroid gland - h					314				173
adipose - h					311				0
prostate - h					309				66
prostate gland - h					307				190
pancreas - h					305				0
ovary - h					303				0
testis - h					302				307
heart - h					298				16
liver - h					297				60
Spleen - h					296				21
apical cord - h					294				111
small intestine - h					292				0
skeletal muscle - h					290				0
bone marrow - h					279				267
adrenal gland - h					277				136
HPAEC					275	275			0
HT302-normal					266				0
HT367-normal					266				85
Base-11					239	239			331
Base-8					235	235			222
HT177-normal					234				0
Base-7					233	233			346
Base-6					231	231			467
Base-5					229	229			82
Base-4					227	227			442
bladder - h					222				80
heart - h					215				0
coracohum - h					214				1006
total kidney - h					213				0
placenta - h					212				123
total brain - h					211	211			0
HCAEC					210				0
HPAEC					209				0
Quadriceps - h					205				267
skeletal muscle - h					203				0
pancreas - h					201				0
testis - h					199				0
Subcutaneous - h					191				48
HEPM 3d TGFB1 antagonist-DHase					193				0
thyroid - h					179				0
WJ-28 T2n					61				0
lymph node - h					59				0
lung - h					57				0
kidney - h					55				0
heart - h					53				0
total lung - h					51				36
total liver - h					49				0
total kidney - h					79				0
HELA-2h-031899					81				524
HELA-0h-031899					80				71
HELA-0h-031899					80				674
HELA-0h-031899					88				57
HELA-0h-031899					90				151
HELA-0h-031899					92				0
HELA-10h-031899					94				81
HELA-11h-031899					96				0
HELA-12h-031899					146				120
NCL-H22N					148				9
NCL-H460					150				66
NCL-H522					152				294
SAB-19					154				0
SAB-75					156				137
SF-269					158				0
SF-295					160				165
OCRP-CEM					162				0
DL-145					164				0
HT-116									0

Table 3¹⁸⁸ (cont'd)

Tissue	Tumor sym	Normal sym	Tumor - 1e	Tumor cells	Normal	Endoc	p53	SEQ 116 S
Cell-1				162				4
766-3				164				0
T-47D				169				0
Ker-3				171				72
CRB1441 RNA B/30				181				0
7817 untreated + DNase				183				169
K562 poly A+				194				47
HOS poly A+				196				0
ACHN				198				52
UACC-67				200				0
MCF-TADR-RES				202				56
UTOS (Mundy) poly A+				204				0
WISH (Collagen) poly A+				206				34
458 muscle mRNA				208				200
COL137 RNA 3/21/88				218				0
WL36 72h 0.5% FBS, 24h 10% FBS				219				0
CRB1441 + TPA (24h) B/30				220				242
Ker-1				221				50
Ker-2				222				79
Ker-3				225				0
MOP-82				241				0
MOLT-4				242				0
U937				243				0
HL-60				244				0
NCL-H23				245				0
RPW8 B226				245				60
A549ATCC				247				241
SR				248				0
OVCA-3				249				85
MCT-15				250				0
OVCA-4				251				0
UO-31				252				0
OVCA-5				253				249
SM12C				254				0
OVCA-8				255				0
LOX BV1				256				0
IGROV1				257				0
SK-MEL-2				258				153
SK-OV-3				259				0
SK-MEL-5				260				0
SP-539				261				0
SK-MEL-28				262				0
K-562				263				72
UACC-257				264				33
M14				265				0
MCF7				267				49
MDA-MB-435				269				169
HT219				270				0
MDA-N				271				0
Y78 poly A+				272				0
KHOS poly A+				289				26
HTB36 72h TPA RNA 6/73				300				147
HELA-EXP-031029				313				83
HTB36 0h RNA				322				0
HT347				323				0
458 muscle RNA				324				125
NCL4226				336				0
MOP-62				337				0
MDA-MB-231				338				61
U251				339				0
PT cells poly A+				340				0
PC-3				341				0
HCC-598				343				0
SW-620				345				0
HT192				346				148
COLO 205				347				0
HT218				348				0
KIA-12				349				0
HT151				350				20
A490				351				0
HT393				352				460
RJF 393				353				0
TK-10				355				363
Mdame-3M				357				241
Pa 5781				359				0
HT213			50					312
HT288			52					0
HT139			54					0
HT155			56					0
HT163			58					165
HT170			60					61
HT172			62					137
HT138			63					0
HT178			64					32
HT154			65					19
HT180			66					40
HT169			67					140
HT185			68					0
HT143			69					0
HT190			70					99
HT145			71					130
HT227			72					151
HT302			73					0
HT314			74					0
HT317			76					0
Basaloid carcinoma 8425 11/8			77					0
HT323			78					21
HT327			80					137
HT335			82					0
HT146			85					98
HT348			87					29
HT311			170					18
HT396			185					0
HT140			187					0
HT281			189					205
HT372			191					75
TCGP			207					40
HT160			216					48
HT307			217					67
HT368			224					254
HT370			226					0
HT371			228					114
HT377			230					125
HT382			236					112
nanucbl carcinoma RNA			281					468
HT334			299					231
HT330			301					0
HT302			315					93
HT394			317					0
HT312			319					0
HT162			325					0
HT395			358					46
HT157			360					13
T-47D	163							63
MDA-N	161							0
MDA-MB-435	159							0
MDA-MB-231	157							30

Table 3¹⁸⁹
(cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - Is	Tumor cells	Normal	Endoc	p53	SEQ ID	118	5
HL-60	150								0	
MCF-7/ADR-RES	153								0	
MCF-7	151								0	
M14	145								0	
UACC-251	147								22	
UACC-62	145								0	
SK-MEL-28	144								30	
UO-31	143								0	
SK-MEL-5	142								91	
SK-M-12	141								4	
SK-MEL-2	140								263	
MCF-15	139								329	
Mammary-34	138								181	
CCL-205	137								250	
LOX-BVVI	136								0	
SW-620	135								0	
TK-10	134								0	
MCF-116	133								0	
T86-O	132								82	
HCC-2998	131								76	
ACHN	130								275	
PC-3	129								0	
RDX-393	128								336	
DLL-145	127								80	
C84-1	126								276	
SR	125								0	
A498	124								137	
RPMD-8226	123								0	
SN12C	122								126	
HE-40	121								0	
MOLT-4	120								118	
OVCAR-5	119								0	
K-562	118								38	
OVCAR-4	117								642	
QCRF-CEM	116								806	
OVCAR-3	115								161	
SF-639	114								87	
HOP-62	113								0	
SF-275	112								161	
ASMBATCC	111								110	
SF-268	110								133	
NCL-H522	109								0	
U251	108								204	
NCL-H460	107								0	
SMB-75	106								38	
NCL-H432M	105								430	
SMB-19	104								78	
NCL-H26	103								62	
SK-OV-3	102								6	
NCL-H23	101								777	
IGROV1	100								0	
EKVR	99								54	
OVCAR-8	98								0	
HOP-92	97								43	
N. Normaliste 3/21/92 #12	48								148	
N. adu. SAMC 10/21/92 #17	47								210	
N. her. monocyt. 2/25/92 #10	46								135	
TCOP	26								0	
AS49-1							wt		5	
AS49-3							wt		379	
AS49-4							wt		458	
AS49-5							wt		347	
AS49-7							wt		73	
EKVR-1							mutant		84	
EKVR-4							mutant		290	
EKVR-3							mutant		0	
EKVR-5							mutant		483	
EKVR-7							mutant		877	
MCF-7-1							wt		0	
MCF-7-3							wt		565	
MCF-7-4							wt		315	
MCF-7-5							wt		0	
MCF-7-7							wt		0	
ADR-RES-1							mutant		3049	
ADR-RES-3							mutant		158	
ADR-RES-4							mutant		79	
ADR-RES-5							mutant		18	
ADR-RES-7							mutant		96	
WI-38-1							wt		0	
WI-38-3							wt		283	
WI-38-4							wt		560	
WI-38-5							wt		589	
WI-38-7							wt		0	
HML-1							HPV E6		0	
HML-3							HPV E6		56	
HML-4							HPV E6		185	
HML-5							HPV E6		308	
HML-7							HPV E6		105	
H1299-1							mutant		0	
H1299-3							mutant		0	
H1299-4							mutant		0	
H1299-5							mutant		0	
H1299-7							mutant		1	
AS49-2							wt		183	
EKVR-2							mutant		0	
HCT-116-1							wt		0	
HCT-116-2							wt		820	
HT29-2							mutant		68	
SF539-1							wt		0	
SF539-2							wt		3	
SF-268-1							mutant		209	
SF-268-2							mutant		631	
OVCAR-4-1							wt		0	
OVCAR-4-2							wt		0	
OVCAR-5-1							mutant		523	
OVCAR-5-2							mutant		208	
MCF-7-2							wt		86	
ADR-RES-2							mutant		221	
HML-2							HPV E6		173	
SW480-1							mutant		0	
SW480-2							mutant		191	
H1299-2							mutant		1003	
C33A-1							mutant		0	
C33A-2							mutant		0	
U2OS-1							mutant		211	
U2OS-2							mutant		557	
Hs68-1							wt		0	
Hs68-2							wt		24	
WI-38-2							wt		299	
Madar-1							wt		0	
Madar-2							wt		0	
Madar-3							wt		0	
Madar-4							wt		14320	
Madar-5							wt		552	
Madar-6							wt		0	
Madar-8							wt		0	
Madar-9							wt		0	

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - te	Tumor cells	Normal	Endos	e33	SEQ 116.3
DafPeng-2								1542
DafPeng-6								2991
DafPeng-9								603
DafPeng-11								2503
DafPeng-12								518
DafPeng-10								368
DafPeng-1								474
DafPeng-3								0
DafPeng-2								222
DafPeng-4								0
DafPeng-5								0
DafPeng-8								0
AS49 - 6							wt	0
ERVX - 8							mutant	56
HCT-116 - 7							wt	0
HCT-116 - 8							wt	0
HT29 - 1							mutant	310
HT29 - 7							mutant	69
HT29 - 9							mutant	0
SF539 - 7							wt	155
SF539 - 6							wt	259
SF-268-7							mutant	218
SF-268-8							mutant	501
OVCAR-4 - 7							wt	405
OVCAR-4 - 8							wt	0
OVCAR-5 - 7							mutant	631
OVCAR-5 - 8							mutant	107
HCF-7 - 8							wt	35
ADR-4E5 - 8							mutant	857
HeLa - 8							HPV E6	0
SW480 - 7							mutant	0
SW480 - 8							mutant	0
HT299 - 8							mutant	0
C33A - 7							mutant	0
C33A - 8							mutant	0
U2OS - 7							mutant	729
U2OS - 8							mutant	37
He68 - 7							wt	0
He68 - 8							wt	0
WI-38 - 8							wt	0
4.5B modula RNA								0
CRL 1572 3/17/89								71
Bev-4						84		221
HT368								80
HT378								151
HT385								80
HT308								0
Bev-3						173		487
Bev-5						175		117
Bev-8						177		481
h keratocytes 2/25/92 #10								0
Bev-10						237		0
HTB10								0
h fibroblasts 3/31/92 #12								0
prostate h								0
huvinc-O5 poly A+								31
SA-C5 (Mundys) poly A+								0
huv poly A+								0
HCT-116 - 3						wt		384
HCT-116 - 4						wt		0
HCT-116 - 5						wt		0
HCT-116 - 6						wt		0
AS49 - 6						wt		0
HT29 - 3						mutant		874
ERVX - 6						mutant		121
HT29 - 4						mutant		540
HT29 - 5						mutant		0
HT29 - 6						mutant		171
OVCAR-4 - 3						wt		339
OVCAR-4 - 4						wt		0
OVCAR-4 - 5						wt		16
OVCAR-4 - 6						wt		0
SF539 - 3						wt		726
SF539 - 4						wt		83
SF539 - 5						wt		0
SF539 - 6						wt		0
OVCAR-5 - 3						mutant		2219
OVCAR-5 - 4						mutant		266
OVCAR-5 - 6						mutant		0
ADR-4E5 - 6						mutant		9
HCF-7 - 6						wt		279
HeLa - 6						HPV E6		371
HT299 - 6						mutant		0
SW480 - 3						mutant		51
SW480 - 4						mutant		0
SW480 - 5						mutant		293
SW480 - 6						mutant		225
C33A - 3						mutant		173
C33A - 4						mutant		162
C33A - 5						mutant		0
C33A - 6						mutant		55
He68 - 6						wt		0
U2OS - 3						mutant		620
U2OS - 4						mutant		561
U2OS - 5						mutant		644
U2OS - 6						mutant		0
WI-38 - 6						wt		0
He68 - 3						wt		288
He68 - 4						wt		821
SF-268-3						mutant		277
SF-268-4						mutant		0
SF-268-5						mutant		125
SF-268-6						mutant		33
DafPeng-13								21
Michell - 20								368
Michell - 21								0
Michell - 22								0
OVCAR-6 - 5						mutant		611
Michell - 10								90
Michell - 11								290
Michell - 12								604
Michell - 13								309
Michell - 14								150
Michell - 15								332
Michell - 16								0
Michell - 17								129
Michell - 18								0
Michell - 19								173

Table 4

Gene Name	SP ID#	na ID#	aa	Family	Group	Length	AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h_beta_adren	H	1	122	AGC	GRK	688		Regulator of G-protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378		PH domain 249-337
AA210825_h	H	9	130	AGC	PKC	978		Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804_h	H	11	132	AGC	PKC	890		Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	448		PX domain 13-120
AA021445_h3	H	32	152	CAMK	EMK	1311		Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h_AAC3348	H	34	154	CAMK	EMK	729		UBA domain 327-365
406786.5_h	H	36	156	CAMK	EMK	1330		PAS domain 133-186, 247-280, 354-386
Z36720_h	H	41	161	CAMK	MLCK	874		WD domain, G-beta repeat 674-711
SGK088_h	H	42	162	CAMK	Trio	2287		Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779
R19772_h	H	44	164	CAMK	Trio	1287		RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528
17000139801197_h_IRA	H	76	195	Other	IRAK	596		Death domain 26-108
AA088547_h	H	78	197	Other	IRE	922		POQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800		SAM domain (Sterile alpha motif) 337-408
AA599286_h	H	89	208	Other	SLOB	649		PX domain 16-122
AA836348_h	H	113	232	STE	NEK	836		Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
PAK6_h	H	115	234	STE	STE20-02	719		P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
SHPFSKQAVEHVQSHLSKKQVTSTLFQOPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV
ELNIHLTMNEFSVHRI IGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVPSEKEMRFYATE
I ILGLEHVHNRVVRDLK PANILLDEHGHARISDLGLACDFSKKKPHASVGTHGYMAPE
VLQKGTAYDSSADWFS LGCMLFKLLRGHSPFRQHKT KDKEIDRMTLT VNVELPDTFSPE
LKSLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVWDWQHVVYLQKYPPLI PPRGEVNAA
DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTTETVYEAVNADTDKIEARK
RAKNKQLGHEEDYALGKDCIMHGYMLKLGPNFLTQWQRRYFYLF PNRLEWRGEGESRQNL
LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKEKLNETFKEAQRLLRR
APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
CFVVYRDLK PANILLDEYGHVRI SDLGLACDFSKKKPHASVGTHGYMAPEVLQKGT CYDS
SADWFS LGCMLFKLLRGHSPFRQHKT KDKEIDRMTLT VNVLQLPDAFSP ELRSLLEGLLQ
RDVSQRLGCGGGGARELKEHIFFKGIDWQHVVYLKYPPLI PPRGEVNAA DAFDIGSFDE
EDTKGIKLLDCDQDLYKNFPLVISERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
EDYAMGKDCIMHGYMLKLGPNFLTQWQRRYFYLF PNRLEWRGEGESRQSLLTMEQIMSVE
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPRA
AILEFSKPPLCHRNSNGL

SEQ ID NO: 124_AA826850_H
MGSSMSAATARRPVFDDKEDVNFDFHFI LRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQ
QCIERDEVNRN VFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
FSEDTVRLYICEMALALDYLRGQHI IHRDVKPDNILLDERGHAHLTDFNIATIIK DGERA
TALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
PGFVPNKGR LHCDPTFELEEMILES RPLHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
MGGNHSKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKMYAMKYMKNQKCI
ERDEVNRN VFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFE
GTVKLYICELALALEYLQRYHI IHRDIKPDNILLDEHGHVHITDFNIATVVKGAE RASSM
AGTKPYMAPEVFQVYMDRGP GYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDVAFKKALMPGF
VPNKGR LNC DPTFELEEMILES KPLHKKKKRLAKNRSRDGTDKSCPLNGHLQHCL ETVRE
EFIIFNREKLRRQQGQGSQLLD TDSRGGGQAQSKLQDGCNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
KLNHKNI VKLFAIEEETTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVS LYGTEEYL
HPDMYERAVLRKDHQKKYGATVDLWSIGVT FYHAATGSLPFRPFEGPRRNKEVMYKI ITG
KPSGAISGVQKAENGPI DWSGDMPVSCSLSRGLQVLLTPVLANILEADQEK CWGFDQFFA
ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHELVYKQTKI ISSNQELIYEGRR LV
LEPGRLAQHF PKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDL DGDASMAKAITG
VVCYACRIASTLLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

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FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCCL

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIIGDVK
LLHIYGYFDEEMAVKYISEVALALDYLHRHGI IHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAPRQDYSRTPGQVLSLSSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDETDTSYFEARNNAQHLLTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPMNSHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFRLRLKRTLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAGHVKLSDFGGLCTGLKK
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRQLAYSTVGTDPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLI GYPPFCSETPQETRYKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENRI GNSGVEEIKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFDDFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSL LPTPALGTPLPIPWVPGSLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHLLTRSRGSRTQGPPGPGGSRVGSRRVPGLPWP PPPHYPAGLPGPSPGPSPP
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNHYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESLPCTAEELSRTTELLPRRPPSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDKFNCHKRCATRVPNDCLEALIN
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEEGGKAQSSLGYP
MRVVQSVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRDLCKCITL FQNNTTNRYKEI
PLSEILTVESAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHKRTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVVMKHLHGDMLEMI LSSEKGR LPERLT KFLITQILVALRHLHFKNIVHCDLKPEN
VLLASADFPQVKLCDFGFARI IGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPSHISAGAILNNLLQVKMRKRYSDVK
SLSHPWLQEQYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

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FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLQIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVLALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNHYHKRCFAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMMVCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSRSSGLDDT
EESPPEDEKMFLLDPSDLDERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLRKRHYWRDLSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIIITDMVYFVGENNGDSSHPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQKGDHKDLSTISVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKLHGDML
EMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSGYNRSLDMWSVGVIIVVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSDKSLSHPWLDQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRHLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQQLQESSQKDLLRLALEQLL
EQLPPAHLPLRSRVTRRELRAAVPGYPQPSGTPVKPTALTGTQLQVRLLGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSPSTISPPKGCPRTR
PTTLREASDPATPSNFLPKKTPPLGEEMTPPKPPRLYLPQEPTSEETPRTRKPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYAIAKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSHARFVTEFVPGGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIIYRDLKLDNLLLDAAQGLFKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M PKNBETA_M

LKWDNLLLLDAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKS LWTGLGTIRSDLEELWELRGHHYHQLHESLKPAVPLVEKPLPEWPVP
QFINLFLPEFPPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR
DTVRQCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

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FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFFTLPDGDASRSFNTSESKVEFKAQ
DTISRGSDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIENKLLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLQFNPLERLGAGVAGVEDIKSHPPFTPVDAELMR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPWREMEVFSGGGASSGEVNLKMOVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA
ELALALDHLHLQLGIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQKDRNETMNMILKAKLGMPQFLSAEA
QSLRMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDDTFCF
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEEYKITPITSANVLPVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEEREASDILYVISKTVDYLHCQGVV
HRDLKPSNIIYMDDESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD
AACDIWSLGLVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPMTKRDYLVDAATQIRLA
LERDVSEDYEAAFNHYQNGVDVLLRGIHVDPNKERREAVKLKITKYLRRAEEIFNCHLQR
PLSSGASPSAGFSSLRLRPRTLSSAVEQLRGCRVVGVIKVLVQDPATGGTFVVKSLP
RCHMVSRLRTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLTPARLPSPGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR
EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSDAGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLISAPEVGGISELTEACDWWSFGSLLYELLTG
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLLGMGEGGVSKLKSHPPFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI
SQPQEPPELMNANPSPPPSPSQQINLGPSSNPFAKPSDFHFLKVIKGSFGKVLLARHKA
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKKQPYDRTVDWWCLGAVLYEMLYGLPPFYR
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQEPPELMNANPSPPPSPSQQINLGPSSNPFAKPSDFHFLKVIKGSFGKVLLARHKA

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FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSEENVLLKNVKNHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNI LNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVSGPSDLRHFDPEFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M

HLQRRERFLEPRARFYAAEVASAI GYLHSLNII YRDLKPENILLDCQGHVVLTD FGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVVSQMY
ENILHQPLQIPGGRTVAACDLLQSL LHKDQRQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKNHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVVLTD FGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNI LHKPLSLRPGVSLTAWSI LEELEKDRQNRLGAKEDF
LEIQNHPPFFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSEDLFL

SEQ ID NO: 143_R47805_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVI EDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGF EWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDL SFAGYQKHLSSCAAPL TSAERELQQIRINEVKTEI SVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIIYSMPGYKCSI KERMLYSSCKSRL LDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFKPKGPGGKRGHKRLIRGPGENGDDS

SEQ ID NO: 144_H60215_H

MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGDQGI ESQEERQGMLLHTEYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS DKTADLINLQHVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVNLKRTHRITITNFCLGKHLVSEGDLLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLF TMLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPQQRLAAADVLEALS AIIASWQSLSSLGPLQVVPDIDDQM
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSI HDTRSWVPKRQFGSAPPVRLGH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H

MASTRSIELEHFEERDKRPRPGSRRGAPSSSSGGSSSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNI KGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK
YKIGKVIGDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

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FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
 RDIKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
 IWAAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
 VNVEARCTAGQILSHPWVSDDASQENNMQA EVTGKLGKQHFNNALPKQNSTTTGVSVMVS
 GRRQVWPDCGAGLEVFELGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M
 TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPGEGVNGNRCSESFPLLEKYR
 IGKVI GDGNFAVVKECVDRYTGKEFALKI IDKAKCCGKEHLIENEVSILRRVKHPNIIML
 VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHLSLSIVHRD
 IKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
 AAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDPCVCFRKCL

SEQ ID NO: 147_AA383293_H
 PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFLEVTSAVQAPLAVRALYTPCHGHPV
 TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPPFSLKLSQAASQDWETVL
 KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA
 GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTKYQQSETSRDGQSFPSGVIGVYGA
 PHRRKETAGALEVADDEDTQTEEPLDQRAAQIVEQVTCLODFFGDDVFIACGPEKFRYA
 QDDFVLDSRRRLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRMTLRDDQPAKLEK
 EPKTRPEENKPERPSGRKPRPMGI IAAVEKHETGRVIGDGNFAVVKECRHRETRQAYA
 MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYILEYVQGGDLFDAI
 IESVKFPEPDAAALMIMDLCKALVHMHDKSI VHRDLKPENLLVQRNEDKSTTLKLADFGLA
 KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPXXGDQDE
 LFNI IQLGHFELPPYWDNISDAAKDLVSRLLVDPKKRYTAHQVLQHPWIE TAGKTNTV
 KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M
 MPTAPVLRPPPPATPAPPAPSRPAPPPIPGHRGPCDHSLKCLSSKISERKLPGPWLPAGR
 GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVVTVVKLGGQPLRKATLLNRRS
 VQTFEQLLSDISEALGFPRWKNDVRKLF TLKGREVKSVSDFFREGDAFIAMGKEPLTLK
 SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
 RHQKGTSTVLAPEDKARAQKWVRGKQSESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
 GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD
 GEEGWKGD SHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGAPKAQKDFVEGPPAV
 EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERRAPE
 KESKRKLEEKRPERPSGRKPRPKGII SADVEKHYDIGGVIGDGNFATVKECRHRETRQAY
 AMKMIDKSQLKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYILIMEYVQGGDLFDA
 IVENVKFPEPEAAVMITDLCKAFVHMHDKNI VHRDVKPENLLVQRNEDKSI TLKLADFG
 AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDE
 LFNI IQVGQFEFLSPYWDNISDAAKDLVRNLLVEDPKKRYTAEQVLQHPWIE MVGHTNTG
 NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H
 MSRRRFDCRSISGLLTTPQIP IKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
 AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
 LCLPELAEMVSENDVIRLIKQILEGVYYLHONNIVHLDLKPQNILLSSIYPLGDIKIVDF
 GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
 QETYLNISQVNVVDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

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FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDDL

SEQ ID NO: 150_W44160_M DRAK2_M

MSRRRFDCRSVSGLLTTTPQTPIKTENFNFFYTLPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNISQVNVYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H

MIPLEKPGSGGSSPGATSGSGRAGRLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEI IHEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVDFT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEI PGFEFIY

SEQ ID NO: 152_AA021445_H

MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNKIIADFGFSNLFPTGQLLKTWCGSPPYAAPELFEGKE
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRI PPFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSAYISLLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGEDEEPSPEALVRYLSMRRTVGVADPRTE
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ
EAVQRYLANRSKRHTLAMTNPTAEIPDDLQRLQGLQPPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNSSIKQLQCECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQPALLTHQLQRLRIQPS
SPPNHPNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQQPAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYPDQAHLPHPLFSDQSRGSPSSYSPT
GVGFSPTQALKVPPLDQFPTFPFSAHQPPHYTTALQQAALLSPTPPDYTRHQQVPHILQ
GLLSPRHSLTGHSDIRLPPTFAQLIKRQQQQRQQQQQQQQQEQEYQELFRHMNQGDAGSL
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSPREPVI GNCMDRSSPGQAVELPDHNLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H

MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTKLDQKTQRLLSR
EISSMEKLHHPNIIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKS ILEG TYSVPPHVSEPCHR
LIRGV LQQIPTERYGIDCIMNDEWMQGV PYP TPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRI ILHRVQRKKALESVPMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487

MSTRTP LPTVNERDTENHTSHGDGRQEVT SRTSRSGARCRNSIASCAD EQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKI IDKTQLNP TSLQKLFREVRIMKI LNHPNIVKLFE
VIET EKTLYLIMEYASGGEVFDYLV AHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLD TFCGSPPYAAPELFQ GKKYDGPVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRG TLEQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLLGRKSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYS
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASNP NK
ADI PERKKSSTVPSSNTASGGMTRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THS ISSAATPDRI RFPRTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
STNLF SKLTSKLT SRNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL D
ANNCDYEQRERFLLCVHGDGHAENLVQWEMEVC KLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M

KGPSWSSRSLGARCNRNSIASCPEEQPHVGN YRLLRTIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIE TEKTLYLVMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLD AEANI KIADFGFSNEFTL
GSKLD TFCGSPPYAAPELFQ GKKYDGPVDIWSLG VILYTLVSGSLPFDGHN LKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNP NKA EI PERRKDSTSTPNNLPPSMMTRN
TYVCTERPGSERPSLLPNGKENSSGTSRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGGVQNGPPASPTLAHEAAPLP SGRPRPTTNLFTKLTSKLTRRV TDE
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H

MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQT TAEP SRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLA AQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLL PAPVCNPNKAI FTVD AKTTEILVANDKACGLLGYSQDLIGQKLTQFFLRSDSDVVE
ALSEEHMEADGHA AVVFGTVVDII TRSGEKI PVSVMKMRMRQERRLC CVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQH IPKNLKI QRSV
GRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALT LFGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGCGER
TLDPWQGGQDPAEGGQDPRINVVL AGGHVVP RDEIRKLMESQDI FTGTQTELIAGGQLLSC
LSPQPAPGVDNVPEGSLPVHGEQALPKDQQIT ALGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCP CYGSEWGLW WRSQDLAPSPSGMAGLSFGTPTLDEPWLG VENDOR EELQTC
LIKEQLSQLSLAGALDVPHAE LVPTECQAVTAPVSSCDLGGRDL CGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLA VGSDPD
VGSLOEQGSCVLD DRELLLLTGTCVDLQGGRRFRESCVGHDPTEPLEVCLVSSEHYA ASD
RESPGHVPSTLDAGPEDTCPSAE EPRLN VQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWL VKDLLHSQRDSAARTR LFLASLP GSTHSTAAE
LTGPSLVEVLRARPWFE EPPKA VELEGLAACEGEYSQKYSTMSP LGSGAFGFVWTA VDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANI I KVL DIFENQGF FQLV

FIGURE 11

MEKHGSGLDLFAFIDRHRPLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDI IHRDIK DEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQVPERRTTLEKLVDPWVTQ
PVNLADYTWEVFRVKNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL
HPGDPRLTTS

SEQ ID NO: 157_AA544838_M 406786_M

TRPHPCLDPLASFIFRQLVSAVGYLHSQGI IHRDIK DENIVIAEDFTIKLIDFGSAAYL
ERGKLFYTFCTIEYCAPEVLIGNPYRGPELEMWSLGVTLYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEVCRTNQPES
GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSLPVS

SEQ ID NO: 158_AA785735_H

MVMADGPRHLQRGPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKI IDKSQLDVN
LEKIYREVQIMKMLDHPHI IKLYQVMETKSMYLVTEYAKNGE IFDYLANHGRLNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLDNMNIKIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRI PYFM
SEDCEHLIRMLVLDP SKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
LRLMHSGLIDQQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHS PNMRLLSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPVPPVLVRKGCQSLPSNMSETS IDEGLETEGEAEEDPAHAFAEFQSTRSGQ
RRHTLSEVTNQLVVM PGAGKIFSMNDS PSLDSVDSEYDMG SVQRD LN FLEDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVHNRS PVS FREGRRASDTSLTQGIVAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPRQSLETQYLQHLRQKPSLLSKA QNTCQLYCKEPPRSLEQQQLQEHRLQOK
RLFLQKQSQLQAYFNQM QIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRRHRYEFLETG
KGTYGKVKKARESSGRLVAIKSIRKDKI KDEQDLMHIRREIEIMSSLNHPHIIAIEHVFE
NSSKIVIM EYASRGDLYDYISERQQLS EREARHFFRQIVSAVHYCHQNRVVRDLKLEN
ILLDANGNIKIADFGLSNLYHQGKFLQTF CGSPLYASPEIVNGKPYTGPEVDSWSLGVL
YILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATR VGEQEAPHEGGHPGSDSARASMA DWLRSSRPLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLKKS RKENDMAQSLHSDTADDTAHRPGKSNLKL PKGILKKKVSASA
EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSES GELL DAGDV FV
SGDPKEQKPPQASGLLLHRKGILKLNKFSQTAL ELAAPTTFGSLDELAPPRPLARASRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDP
LGDSCFSLTDCQEV TATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H

MPAAAGDGLLGEPAAPGGGGGAEDAARPAACEGSFLPAWVSGVPRERLRDFQH HKRVGN
YLIGSRKLGE GSF AKVREGLH VLTGEKVAI KVIDKKRAK KDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLDENNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNMYAMLTGTLPTVEPFSRLALYQKMVDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVP CNVTYPNRISLEDLSPSVVLHMTEKLG YKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKPKKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSNSCVASSSMEFIPVPPPTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGMSPLHTPLHPTLVSFHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLOPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNLNLEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAEERLPPIRASGLG
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPCGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHIQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQOGKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVSVKETSISAGYEVCOHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSADREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKI IDFG LARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVI TYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCMSATQCLKHEWLN NLPKASRSKTRLK
SQLLLQKYIAQRKWKKH FYVVTAA NRLRKFTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLT SVHEDDSGVYTC
KLSTAKDELTC SARLTVRPSLAPL FTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEES ENLRLRQDGG LHS L HIAHVGSEDEGLYAVSAVNTHGQAHC SAQLYVEEPRTAAS
GPSSKLEKMPSI PEEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNHGR IQSSDDRMTQYRDVHRLVFP AVGPQHAGVYKSVIAN KLGKAACYAHLYVTDVV
PGPPDGAPQVVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQH QVLGSDQWTALVTGLRE
PGWAATGLRKGVQHI FRVLSTTVKSSSKPSPPEPVQLLEHGPTLEEAPAMLDKPDIVYV
VEGQPASVTVTFNHVEAQVVWRSCR GALLEARAGVYELS QPDDDQYCLRICRVSR RDMGA
LTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQN LAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHRRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSQAKPKAS
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLER IARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCYGTP
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDR TTMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP
EFGSGRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEA PSPEALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGP GATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLESLGGRARDPRMARAASSEAPHHQPPLE
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP
SAPKPSTPKSAEPSATT PSDAPQPPAPQPAQDKAPEPRPEPV RASKPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGPAAAPPSEP KPHAAVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSSLSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT P
PAQRHPAWEARGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQ RSGSSSEDSSGGAS

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FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPVFHIIKLKDQVLLEGEAA
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCDKGRQLLSIPRAGKRHAGLYECSATN
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
 HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSSLKAVGPP
 PQTPPRRHRGLQAARPAEPTLPSTHVTPEPKPFVLDGTGPIPASTPQGVKPVSSSTPVY
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
 PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQOEYEVLRTLHHER
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFYSEDDVATYMVQLLQGLDYLHGHV
 LHLDIKPDNLLLAPDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLSV
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLLR
 SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
 ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLS
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLL
 RSYPGSP

SEQ ID NO: 164_R19772_H
 MKGGDRAYTRGPSLGWLFACCCCFPCRDAYSHSSSENGGKSESANLQAQPSLNFIHSS
 PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIKKQKKVRDGRKSFDLGSPKPGDETTPQGDS
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA
 IEKLVKNKLSLEGSSYRGSCLKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVLNELV
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
 QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVA EYDAYFEEVKQEINQRLTLSDFLIK
 PIQRITKYQLLLKDFLRYSEKAGLECSDI EKAVELMCLVPKRCNDMMNLGRLQGFEGTLT
 AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN
 YLVLEENVNDNDPCKFALMNRETSEVVVLOANADIQQAWVQDINQVLETQRDFLNALQSP
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPLKISTSNNGSP
 GFEYHQPGDKFEASKNDLGCGNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQNMCMC
 LUYQPASDHSPAAEGWVPGSILAPLTKATAAESDGSIKKSCSWHTLRMRKRAEVENTGK
 NEATGPRKPKDILGNKVS VKETNSSESECEDDLDPNTSMEILNPNFIQEVAPFLVPLVD
 VTCLLGDTVILQCKVCGRPKPTITWKGPQDQNILDTDNSSATYTVSSCDSGEITLKI CNLM
 PQDSGIYTCIATNDHGTTSTSATVKVQGVPAAPNRP I AQERSCTSVILRWLPPSSTGNCT
 ISGYTVEYREEGSQIWQQSVASTLD TYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATR KDVAVKFNKMM
 KKKEQAAHEAALLQHLQHPQYITLHDTYESPTS YILILELMDDGRLLDYL MNHDELMEEK
 VAFYIRDIMEALQYLHNCRV AHLDIKPENLLIDLRI PVPRVKLIDLEDAVQISGHFHIHH
 LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLT YVMLSGVSPFLDESKEETCINVC RVDFS
 PHEYFCGVSNAA RDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
 ERRKHQNDVRPIPNVKS YIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H
 MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLVVEMSQTSSIGSAESLISLERK
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFT EGKVPHIRIENGAAIEEIIYTFGR
 ILGKGSFGIVIEATDKETETKWAIIKKVNKEKAGSSAVKLLEREVNIIKSVKHEHIIHLEQ
 VFETPKKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
 LENIMVKSSLIDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

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FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGE LHFENAVWNSI SDCAKSVLKQ
LMKVDP AHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEK NKPS
TEEKLKSYQPWGNVPETNYTSDEEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPTVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDETMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
VALKVESAAQQPKQVLKMEVAVLKKLQSGSLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIIHVSGLHHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKEYEHRMMLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPISLLARPLF
PVPSPALASLCLPSSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQQPKQV
LKMEVAVLKKLQGDHVCRFICGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHNRNEMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRMLMLKHLPPFEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFGARAKSIPSQYSSSEVVTWYRPPDALLGATEYSSSELDIWGAGCI
FIEMFQGGQPLFPVGSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
AYTDYVATRWRAPPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVDVHPVALNFMKGCLKMNPDDR
LTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQLK
FDHLPNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLI EVFRRKRKMHLVFEYCDHTLLNELERNPNNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATRWY
RAPPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQ
SIFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDERLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKKGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHKSKHSDMGLVTPEA
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDDLHKHRHHQHRRSR

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FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRI SGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSOSSKQDDSPSGA
SYGQDYDLSPSRSHTSNNYDSYKKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRRSSSYERSGSGYSGRSPSPYGRRRSSSPFLSKRSLRSRPLPSRKSMKSRSRSP
AYSRHSSSHSKKKRSSSRSRHSSISPVRPLPLNSSLGAELSRKKKRAAAAAAAKMDGKES
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTTEVKNSSDTGK
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPPLPTIASPPPLP
TTTPPPQTPPLPPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSASVSSQAN
SQPPVQVSVKTQVSVTAIIPHLKTSTLPPPLPPLPPLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPPELPGGDLSPDPSPEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ
LIHRSVVMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLGLESGLVHFSEDHIKFSM
KQLMEGLEYCHKKNFLHRDIKCSNILLNNSGQIKLADFGGLARLYNSEESRPYTNKVITLW
YRPPPELLLGEERYTPAIDVWSCGCGILGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPDLPWHQDCHELWSKKRRRQSQSGVVVEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDL SIPQMAQLLNI
HSNPEMQQLEALNQSI SALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPHHEH
QALRPMYESTRPRPNRTYGN TDGPETGFS AIDTDERN SGPALTESLVQTLVKNRTFSGSL
SHLGESSYQGTGSVQFPQDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVHAETKLQNY
GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVY

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLI EVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRRLKYL FQILRAIDYLHSNN
VI IHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG
KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAKVNSLI
KPKESKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDI SEP
KKKEYEGGLGQDANENVHPMSPTDKLV TIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSDQMANENKRKLNF SRSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNQEQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLQIDPAERTSSTDLLRHDFYTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN
FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRTSSQTIGQTLNSNRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFGGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFPGENDIEQLCCVLRILGTSPSRVWPEITELPDYNKISFEEQAPVPLEEVLP
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
GPPHVHDFHVDRIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H

MITSI STEKSGH THYPFMITTLQYYRGRGGKTAVVRHFS AEGPF AFAEMRHSKRTHCPDW
DSRESWG HESYRGSHKRKRSHSSTQENRHCKPHHQF KESDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSR SXEIV
DTLGE GAFGKVVECIDHGM DGMHVAVKIVKNVGRYREAA RSEIQVLEHLNSTDPNSVFRC
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVVD FGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ
KTRKRKYFH HNQLDWD EHSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNIISLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGGGL
LQDVHVRSIFYQLLRATRFLHSGHVHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATR WYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL
QHYPVQRFHCP SDEWAREADVRPRAHEGVQLSVPEYRSRVYQMILECGGSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGP RP RPQSSPGHDP AEHES PRAAKNVPRQNSAPLL
QTALLNGERPPGAKEAPPLTSLSVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFST SALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFD RKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLT DGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILTKFKQSRAMNFD FP
FKKSGSIPLLTTNLSPQCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGSGTNGRVPVLRPLKCI PASKKTD PQKDLKPAPQQCRLPTIVRKGG R

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGTYGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFIHKLG
FFHRDLKPENLLCMGP ELVKIADFG LAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKTDWPEGYQLSSAMNFRWPQ
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQP PPAKPHTRISSRQH QASQPPLHLTPYKAEVSRTDH
PSHLQEDKPSPLLP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGN SAPTQT SYQRRDTPT
LRSAAKQHYLKH SRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISKVNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQVRHLAPIPD PSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGGMSAE E EIGPGAEPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKD HAAQ
GPGRTEAGRVSSAAEAAI VVLDDSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKI IKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

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FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCMSATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKHFFHVVAAVNRLRKFP T C P

SEQ ID NO: 180_AA460132_H

MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFLLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H

QREKVNQGNMPGLQSTFLAMDTEEGVEVVWNEHLHFGDRKAFAAHEEKIQTTFEQVLVLDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTCKKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTRVTEEA I ARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM
DLHAVLAELPRPRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMOCNLERSEDKARWHLTLLLVLLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLA AFLESTFLKYRG TQA

SEQ ID NO: 182_AA103218_M SGK034_M

HASAPEYGEVNDGTGFVDIFSFGMCALEMAVLEIQANGDTRVTEEA I ARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLFVHSLKLLAAHCFIQHQYLMPENNVVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAP
PEEAQKAKTPTPEPFDSETRKVVQMOCNLERSEDKARWHLTLLLVLLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRTKLA AFLETTFLKYRG TQA

SEQ ID NO: 183_NEK7_H, N34132_H

MSGGAAEKQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPP
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAWCELQDRKLT KSERQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLI IHRDLKCDNIFITGP
TGSVKIGDLGLATLKRA SFKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLNHAF FQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLQKQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEPEADQHQQQLQYQQPSISVLS DGTVD SGQG
SSVFTESRVSSQQT VSYGFPXHEQAHSTGTVP GHI PSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQT VQYSL SQTSTSS EATTAQPV SQPQAPQVLPQVSAGKQSTQGV SQVAPAE PVAV
AQ PQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGR TTKRHYRKS VRSRSRHE
KTSRPKLRILNVS NKGDRVVECQLETHNRKMVT FKF DLDGDNPEEIATIMVNDFILAIE
RESFVDQVREIIEKADEMLSEDVSVEPEGDQGLESLQKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQAFSELRAQMTEGPNTAPPNFSHTGPTFPVPPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVTSGGLPIPPVSESPVLSSV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
LPQVPSIPPLVQPVANVPAVQQTLIHSQPQAPALLPNQPHTHCPEVDSDTQPKAPGIDDIK
TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
TNLPLGTVALPVTVPVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL
PSEQLPFPFGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSAVGPVSMAAPTAITEAGTQP
QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPPKEKEPELSEPSHLNGPSSD
PEAAFLSRDVEDDGSGLSPHSPHQLSSKSLPSQNLQSLSNSFNSSYMSSDNESDIEDDLK
LELRRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPVPAVIPPAAPLSGRRRRRPTKSKGS
KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLLHPPGNIPESGQNQLLQPLKPSPSSDN
LYSAFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSGSDPKVESSSSAPGLTSVSPPVSTTSAASPEEEEESEDESEILEESP
CGRWQKRREEVNQRNVPIDISAYLAMDTTEEGVEVVWNEVQFSEKKNYKLQEEKVRAVFDN
LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTCKKNHKTMEKAWKRW
CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHNKTCREEQKNL
HFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNGGESSYVPQEAISSAIQILLEDPLQ
REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNM
DTSAVLAEIPAGPGREPVTLYSQSPALEDKFLDVRNGIYPLTAFGLPRPQQPQQEEV
TSPVVPSPVKTPTPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
MPNENIPELAAELVQLGFISEADQSRLTSLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKTCKKNHKTMEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
IGSVAPDTINNHNKTCREEQKNLHFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNG
GESSYVPQEAISSAIQILLEDQLREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLA
AHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVTLYSQSPALEDKFLDVR
NGIYPLTAFGLPRPQQPQQEEVTSPVVPSPVKTPTPEPAEVETRKVVLMQCNIESVEEG
VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLEETLNK
FNFTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKSGYGVVK
LAYNENDNTYYAMKVLSSKKLIRQAAFRRPPRRGTRPAPGGCIQPRGPIEQVYQEIAIL
KKLDHPNVVKLVLEVLDNEDHLYMVFEVLNQGPMVEVPTLKPLSEDQARFYFQDLIKGI
EYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTAPFMAPESLS
ETRKIFSGKAKDVWAMGVTLVCFVFGQCPFMDERIMCLHLSKIKSQALEFPDQPDIAEDLK
DLITRMLDKNPESRIIVPEIKLHPVWTRHGAELPSEDENCTLVEVTEEEVENSVKHIPS
LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
PGHRPAPRGGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
QTFNKEIKTMKKFESPNIIRIFGICIDETVTPPQFSIVMEYCELGTRELLDREKDLTLG

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FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGT
REKTDVVKSTAYLSPQELEDVIFYQYDVKSEIYSFGIVLWEIATGDI PFQGEEDWLSQW
L

SEQ ID NO: 188_H85811_H

MAPVYEGMASHVQVFSPHTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSLPYEQTIVFPGSTGHIIVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDYQKCGCLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWRGTNEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKHNTCLVFEMLEQNLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSGLIHADLKPENIMLVDPSPRPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTSPPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLGSDMLVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLDDFPHSTH
VKSCFQNMIEICKRRVNMVDTVNQSKTPFITHVAPSTSTNLMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAIICARPDFFQQAALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAQWPSGTQQIILLPPAWQQLTGVAHTSVQHATVI PETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAQAQPLNVGVAVHMRQQPTSTTSSRKSQKH
QSSVRNVSTCEVSSSQAISSPQRSKRKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPPYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDLSV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITRQQRPGPHFQQQQPLNLSQAQQHI
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTGYPPLSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQGKSSDCLNTVKSNSSSSKAPKVPLTPEQALKQYKHHLT
AYEKLEIINYPEIYFVGPNACKRHGVI GGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKLRYVALKMVRNEKRFHRQAAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMAFELLSIDLYELIKKNKFQGFVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMMELLMGPPPKLLEQSKRAKYFINSKGI PRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGDDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRPLTTIDKVSGRVVNPASAFQGLGSKLPPVVGIAANKLKANLMSETNG
SIPLCSVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M

TRPELLGMPPQKLLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPPG
SKDWATAKGC GDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGR
VVNPTNAFQGLGSKLPPVVGIAASKLKANLMSETSGSIPLCSVLPKLIS

SEQ ID NO: 191_5R72_16_2_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY
PQGLTGEEVYVKVDRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ
RRKEEIKEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNKGHR
ANSSGRSRRERQYSVCNSEDSPGSCIEILYFNMGSPDQLMVHKGKICGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPFLLTSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

FIGURE 1R

YLAMNLEQDDSI VVDILVEHISGVSLAAHLSHSGPI PVHQLRRYTAQLLSGLDYLHSNS
VVHKVLSASNVLDVAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLLSLSQGECEYPTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSRLPSAAFFSETQRQFSRYFIEFEELQLLGKA
FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYNAWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVEWSTSGERSAS
ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSEDIIFDNEDENSKSKNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG
MVG TALYVSPEVQGSTKSAYNQKVDLFLSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPPQMEESSELHEVLHHTLT
NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIITYIYEIIQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSNSLCLRLYKF
IEQKGDLOQLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
VQQHNGIIFQFVAFIKRRQRAVPEILAAAGGRYDLIPQFRGPQALGPVPTAIGVSIADK
ISAAVLNMEESVTISSCDLLVSVSGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVHDVLQKLRTKVTDERNG
READSNLAVQNLKGSFSNASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H

MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSLRHH
NRAITHLMRSAKERVQRQPCEDISRIQKIRSREVALEAQTSTRYLNEFEELVILGKGGYGR
VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLLRNNSHLEESFTSTEE
SSEENVNFLGQTEAQYHMLHLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELFFQPFQTEMERA EVLTGL
RTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLQMKIIEQ
EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193_17000057519457_H

MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFLSTHPNTETVFEAFKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRTVQEARALLRCRRAGIA
APVVFFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARMGQVLAMHDQD
LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVLDLYVLEKAFLSTHPHTETA
FEAFKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
YVDQGKSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPHENEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKMKQCKKHWRFLSELEVLLLFHHPNILELAAYFTETEFKFLI
YPYMRNGTLFDRLOQCVGDTAPLPWHIRIGILIGISKAIHYLHNVQPCSVICGSISSANIL
LDDQFQPKLTDFAHMAFRSHLEHQSCINMTSSSSKHLWYMPPEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSFDDKKVPPCPRNFSKLFCL
LAGRCAATRALKRPSMDEVLTNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPEKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRFLSELEVLLLFRRHPHILELAAYFTETEFKCLVYPYMSNGTLFDRLOQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPPEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRGDLSCLSFDRKIPPCPRNFSKLFSLAGRCVATKAKLRPTMDEVLSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHVSPPKEVLGTDRTVQK
TPFECSQSEVTFGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYSGKPMKRCSSGLFCSEHEQSKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLLGTLSQPQVHTLRPENLLLSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQGLMKLPFTIPELVHASPCRSS
DGVFYTGKQDAWFVVDPESETQMTLTTEGPSTPRLYIGRTQYTVTMHDPAPALRWNT
TYRRYSAPPMGSPGKYMSHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL
RQLPHLTARDTLHFLALRWGHIRLPASGPRDTATLFTSLDTQLLMTLYVGKDETGFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPSGSVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLRLRECFLVRREVQLLQESDRHPNVRLRYFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPDSQGLGRVVLSDFGLC
KKLPAGRCFSLSHSGIPGTEGWMAPELLQLLPDSPTS AVDIFSAGCVFYVLSGGSHPF
GDSLRYQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVS DWLEKESEQEPLVRALEAGGCAVVRDNWHEHIS MPLQTDLRKFRSYKGT
SVRDLLRAVRNKKHHYREL PVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES
LFLPYYPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGG
KSLNDLIEERYKASQDPFPAAILKVALNMARGLKYLHQEKLLHGDIKSSNVVIKGDFF
TIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVIITDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDDEKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIIGYRAFTEASDGSL
CLAMEYGGGKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLKYLHQEKLLHGDIKSS

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FIGURE 1T

NVVIKGFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENC GGSGSVYRAKWISQDKEVAVKKLLKIEKEAEILSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWWAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRCIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWWVQQLVRKGDSSAE
MSVYASLFKENNITGKRLLLLLEEDLKDMGIVSKGHIHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFNT
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSRNRKYGRGSIISLNSSPRGRYSQSGHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSRDLHQPNITPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNI FGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLH
FCSRFGHHDIVKYLLQSDLEVQPHVUNIYGDTPHLHLACYNGKFEVAKEIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQRDGHGTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLPSHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIFVGAACLNPSQFAIVTQ
YISGGSLSFSLLEHQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNIILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLOQYTPIDKYGYVSDPMSSMHFHSRNSSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLECLQSLEKSQDVSVHITSNYLKQILNAAHYVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRLQDVLHLRKPGLG
QELGRGQYGVVYLCDNWGGHFPALKSVVPPDEKHWNDLALFHYMRSPLPKHERLVLDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLTYGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLNVLDDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGIVQPMQLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRPSPQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGVPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQPNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAACHLKT
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPFTT
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQOTLHSTLLNPIPKCRPALCTLL
SHDFFRNDLFLEVVNFLKSLTLKSEEEKTEFFKFLDRVSLSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLLSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSVDKNTSEDSNFSSSKKSEEPDWSE
PEEPENQTVNIQIWPREPCCDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPKVDPEMDWFADMIPEIKPSAAFLILPELRTEMVPPKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVKNQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLQFQDNLQKSQFFKGLPKVL
PKLPKRIVIVQRIPLCLTSEFVNPDMPVFPVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTKTTPDEIKNSVLPVMYRALEAPSIQIQELCLNIIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNILAYIDGLETEKCLHVVTAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNNGGPPRKGIP
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWVFNGLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLLEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPLQLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVHGFDTNPATIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEEVEKDVHAASSPGMGAAASWAGWAVTGVSSLTSLKIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPPPDGTR
LASEYNWGGPSSDKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

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FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFRRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSKDFQCLIKLLPSCLPYIYRVTFATANESSALLIRMFNEKGTLDKLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLLHASNVMLDGD
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPPLFSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQQIHHQHRRLTRAQSHHGSEERKKRKILARKKSKRSALENSEEHSA
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSAEASCLHLEGKVLFFYSYSPLPPN
YPLPGKVIAEPVQPQTVLFCRCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGDSGGSGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNTRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVSAGHYTETA
VDEIKLLKCVRDSDPSDPKRETIVQLIDDFRISGVNGVHVCMLVLEVLGHQLLKWI I KSNY
QGLPVPCKVSIVRQVLHGLDYLHTCKKI IHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRDLQRLEAMEAATQA
EDSGLRLDGGSGSTSSSGFSGLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGGPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN
LKHGWGLYEVLMKEYEWPLEQATQFSAFLPLPMEYIPEKRASAADCLQHPWLN

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTLDDHKNIIQVYEMLESADGKICLVMELEAGGDVFDVLCVNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFLNKLTDGFGAKVLPKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTLDDHKNIIQVYEMLESADGKIYLVMELEAGGDVFDVLCVNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFLNKLTDGFGAKVLPKSRRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAIFYTKQKVMVAVKIISSKKK
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQTLTGIAYLHKSISVHRDLKLENLLDKWENVKISDFGFAKMPVSNQPV
GCSXPYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPLF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLEFIKCGALHEDVARKMFRLQ
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

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FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQRLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHS GAIEVGKAST

SEQ ID NO: 214_AA883975_H

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRPHPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQNRGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSTTYCGSAAAYASP
EVLLGIPYDPKKYDVWSMGVVLYVMVTGCMPPDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H

VGRQETGVRRWAFLICQPISPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG
KICLVMELAEAGGDVFDVNLGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PXKMLWQQQKGVSFPTH
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216_H29974_H

YSLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAE EPCYLWFMFCEGG
DLNQYVLSRRPD PATNKS FMLQLTSAIAFLHKNHIVHRDLKPDN ILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M

PLLLPPPPAAMETGKENGARRGTKSPERKRRSPVQRVLC EKL RPAAQAMDPAGAEVPGEA
FLARRRPDGGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAE EPCYLWFM EYCEGGDLNQYVLSRRPD PATNKS FMLQLTSAIAFLHKNHIVHRDLK
PDN ILITERSGTPILKVAD FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H

MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFMVD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFHKNQIIHRDLKPDN ILISQTRLDT
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM
NGRMKQLIKEMLAANPQDRPD AFELELRVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H

MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGS GTYATVYKAYAKD TREVVAIKVAKKSLNKASVENLLTEIEILKGIRPHPHIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

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FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H

MENFILYEEIGRGSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT
FHEWYETSNHLWLVLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMSRVKGSVPYTAPEVVRGAD
FSISSDLWSLGLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQORDPQKRLTWTRLLQHSFWKKAFAAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPRTSTAVEV
SPGEDMTHCSPQKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPFLQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPVPRQCLVYV

SEQ ID NO: 221_SGK384_H

SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M

MGQQHGTRNGLTHRELPRGVGLLAMALMNVALYLCLDQLFISPGRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGV
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPQSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLDIHKACKSQIPAERPTAQNVLDAYQRFHSLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H

EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALLEYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNI RAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMGDTEAMHLRKSRLRQSPGSLKAVLKTMEEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLMHMDQWLSQDQDRVPGKRDFA SLGKLGKLLGPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESLSEELQNAAGLLEHILEHLNSSLERSDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVALLQSIIRLCQDRALLVNNAYRGLASLVKV
SELA AFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEI KERFTSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M

EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEEKQIPGTDVYYLLLPFMLHINPSDLAIKDVMQVTFMSNSFKSSSV ALNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVND SRHCD SGIGSQRLGDFQSVSWTEHPLKD
VMQNFSSRPEVQLRAINLLTMPEDQLGLPWPTELLEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLSIQLCPGRVLLVNNAFRGLASLAK

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FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLGRGPAGRRAEPPRSLSRPGPGPGSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQRALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDI PDTLTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLD SI VNATGE
LAWGVDETLAQLEKVLHLRYSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFFVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGI PDTLTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLD SI
VNATGELAWGVDETLAQLETALHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFFVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSRPLSLFSDGDSSESEDTLSSSERSKSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
YEAAPTSTLTCDSPQKQKFSCLKDAKDGRLFNEQNFFQRAAKPLQVNKWKLYSTPLLA
IPTCMGFGVHQDKYRFLVLP SLGRSLQSALDVSPKHVLSERSVLQVACRLDDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVMALTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLDDALEYLHEN
EYVHGNLTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMVP

SEQ ID NO: 229_AA45427_H

MGHALCVCSRGTVIIDNKRYLFIQKLGEFFSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRLFNHPNILRLVAYCLRERGAKEAWLLLPFFKRGTLWNEIERLKDKGNFL
TEDQILWLLLGICRGLEAIAHAKGYAHRDLKPTNILLGDEGQPVLMDLGSMNQACIHVEGS
RQALTLQDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVL YAMMFEGEPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRPHIPLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

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FIGURE 1Z

AVSACQEIQAIF TQKSKPGPDPLDTRRLQGRLEEYLIGQSIGKGCSAAVYEATMPTLPQ
NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE
LVPASRVALAGEYGAVTYRKS KRGPKQLAPHPNI IRVLRAFTSSVPLLP GALVDYPDVLP
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTPSRPLAAMMLLQ LLEGVDHLVQQGIAH
RDLKSDNII LVELDPDGC PWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGKAHLESRSYQEAQLPALPESVPP
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQAATLL
ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H

MEKYERIRVVGRGAFGIVHLCLRKADQKLVI IKQIPVEQMTKEERQAAQNECQVLKLLNH
PNVIEYYENFLEDKALMIAMEYAPG GTLAEFIQKRCNSLLEEETILHFFVQIILLALHHVH
THLILHRDLKTQNIILLDKHRMVVKIGDFGISKILSSKSTPCYISPELCEGKPYNQKSDIW
ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQGIIMTFGSGSNGCLGHGS
LTDISOPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTAHSAAVTGEEDL
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPPDKCCWRHKQCTGHI IYPFASDCV
RHS LHLHSVNHNCNSRLKDSSSEDSSSSRGAGPTCSHVIESPCFELTPEEEEHVERFRYGW
CKSYRPVSVAVIHHPLYHECGADDLNKKRKR RRRRSKPPIPTQVGPATASPD LGTSMAT
GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
KKSPVKLEPSPPDVSRSL SARQLARMSESSPESREELESEDSYNGRGQGELSSEDI VESS
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H

MSVLGEYERHCDSINSDFGSESGGCGDSSPGPSASQGPRAGGAAEQEELHYIPIRVLGR
GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEIVILALLQHDNI IAYYNHFM
NTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
NIFLTKANLIKLG DYGLAKKLNSEYSMAETLVGTPTYMSPELCQGVKYNFKSDI WAVGCV
IFELLTLKRTFDATNPLNLCVKIVQGI RAMEVDSSQYSLELIQM VHSCLDQDPEQRPTAD
ELLDRPLL RKRRRSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
NTHFAVVTV EKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQ GKAI RQVSCGDDF
TVCVTDEGQLYAFGSDY YGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHV VVLT
R NKEVYSWGCGEYGR LGLDSEEDYYTPQKVDVPKALII VAVQCGCDGTFLLTQSGKVLACG
LNEFNKLGLNQCMSGI INHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTTAAID ERGR
LLTFGCNKCGQLGVGN YKKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQQES ETPDPSSGFRGTMEADRGMEGLISP
TEAMGNSNGASSCPGWL RKELENAEFI PMPDPSPLSAAFSESEKDTLPYEELQGLKVA
SEAPLEHKPQVEASVTELF AFESQLVTSAESCSNLCWEGNTTDS SCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H

MNLLLSYRDVQDYS AIIELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV
LLPLVQLEGSVAPDLYCMGRIYKDMFFSSGFQDAGHREQAYHWYRKA F DVEPSLHSGIN
AAVLLIAAGQH FEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLG AQILANDPTQV
VLAAEQLYKLNAPIWYLVSVMETFLLYQHFRPTPEPPGPPRRAHFWLH FLLQSCQPFKT
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTD PVSTVTL SLLEPETQDIPSSWTFPVASICG
VSASKRDERCCFLYALPPAQDVQLCFPSVGH CQWFCGLIQAWVTNPDSTAPAEAAEGAGE
MLEFDYEYTETGERLVLGKGT YGVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWG PLKDNESTISFYTRQILQ
GLGYLHDNHI VHRDIKGDNLINTFSGLLKISDFGTSKRLAGITPCTETFTGT LQYMAPE
IIDQGPRGYGKAADIWSLGCTVIEMATGRPPFHELGSQAAMFQVGM YKVHPPMPSSLSA

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FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAAVLEQEELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRRLRAQGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSLLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLITYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGPSNFEHRVHTGFDPEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKETSINGLLEDFDNISVTRSNSLRKESPPTPDQGASSHGPGHA
EENGFITFSQYSSSEDTTADYTTEKYREKSLYGDDLDPYRGSHAQKQNGHVMKMKHGEA
YYSEVKPLKSDFARFSADYHSHLDSLSKPSYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNTSPQPTMRQRSRSGSGLQEPMPFG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKLQPS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPSPSWGSSS
DQQPSRVSHQFRAALQLVVSFGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVDMYSSYLVGDELWVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVHRDIKSDSILLTSDGRIKLSDFGFCAQVSKEVPKR
KSLVGTPYWMapevisRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRRIRDSL
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEIICRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSEAGHGNGVALPLKETSVENFLGATTPALAKLQ
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIQF
HQYLGKHKNLVQLEGCCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRLPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLTTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLVLQQLRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYVNGGE
LFFHLQORERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLHLKQDQRQLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

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FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS
PLFP GKNDIEQLCYVLRILGTPNPQVWPELTELDPY NKISFKEQVPMPL EEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTA PLPAHPSELPI PQRLGGPAPKAHPGPPHIH
DFHVD RPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLP GFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFP PRVERLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFSRLTRLD DFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLI KRDENGYSAVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEI IARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKI PHKSPCPRRTIWLSRSQSDIFSRKP
PRTVSVLDPYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRS LPGSPEFLHQEACPFVGREESLSDGPPPRLLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF
STSGIGLQTQ GKQDG

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FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTCTTCTCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCACTAGATTTTGTGCTAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCACTGTGCATAGGATTATTGGACGAGGA
GGATTTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTGTCAGCACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCCTGC
GATTTTTCAAAAAGAAGCCTCATGCGAGTGTTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACCTTCTGAGAGGTCACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCTCCCGGGGAGAAGTCAATGCTGCT
GATGCCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAAATGCATT
TTGTTTCAGAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGGAAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCCTCAACAAACCTCGGTCAGGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGACAGCTTCCAGATGCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

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FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTTACCTGTTCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCCAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCTGAAGGAGGGGCCAGCTCTTCAGCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCTTGGTGAACCTCTGGTACTCCTTCCAGGACGAGGAGGA
CATGTTTCATGGTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCAAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGAGATCTTCCAXTCTTT
TGTCAACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTCCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTGCCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCGTGGTCCCTACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTACAGTTCCACCCAGCCTGGCTGGCGGT
GCCCCAGTGGCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTCGTGGGCCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCTTGACAGCAGAGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA
ATTTCTGTATAGTTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCCGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

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FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTAC
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTCACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAACCTT
TGATATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCGCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACCTTCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCCC
ATCCAACCTGGCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAACCTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTTACAGGAGGAAAATGGGTTTACACAAAAAGCAAACCTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTCAGTTTTTCTGTGCAAAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTTCATCCAACCTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTATCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGACACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCTGTTCAAGT
TGGCATTTCTTGTGTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCCGCGGCGGTGGCGCGGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTG
CATGTGGGAGTTTATACACTGTTTTAGAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAGTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTTGCAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTATAGCTATA
ATACTGCTACTATATTTTATGAAGTGGTATATAAACAACCAAAATTTATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAACCTACTGAGGAAAACCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAACTGTTCAAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTTCAGACATACACACCAAATTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCCTGTTAAATTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTTGTATTTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCCTTTATAGATAGTCACTTGTTTCTACAATCCAGTATTTGATGTGGTCG
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCCTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTACAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTA AAAACTATTC
ATTTTTTTCCTTTGGCCATAAATGTGTAATTGTCATTAAAATTCTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCCTGGCACTAAGCAAAAGCCCATTCAATTGTCCATTTGTATTATTTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTACGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTCAATTTCTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGACGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAACCATTTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAACTTGTGA
TATAGAATTAAGTTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG
AATTAATAACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTTATCCATCG
GGATATTAAGCCAGACAACCTTTTTATTGGATGCCAAGGGTCATGTAAATTTATCTGATTT
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAACAGAAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAAGTGCCAAATACCACAGAACCAGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGTCTATTGACTACAAGAGGAAATTTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAACACCTCTAATCAATTCAGGAGAAACACATATCATTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTAGAACATTGCCCTATTGGTTTGGACATC
TGTAAGATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG
TGACAAGTTTATAATAAGGAAGACAAAGTTTAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTACAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAACTTCTT
TTTTTAACAAGAGGACATGGCATTATTTTAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAACTATTTTTTTAAATGTC
AACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAATTTTTCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAGATCTT
GAACAGAGTGGATGTTTCAACTGAGTAGAATTTTCTTTCTGTGGGCATGCTGTATTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCTAATC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTTATAAATGATCTATGA
TCAAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCCATTTTTTGGTTTTGTTTCTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATACTGCCTTTAATTAACATAATATTAATTTTGCTGAGGTT
TATGAGATTTTCTCACCACATCGCTCCCCTTTTTTTAAAGGACTGTTTGTCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTTCTAGTATGGTAA

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FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTTTAATTGCATAATAGAGCATTTTTTGTGTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAAGCATTCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAAC
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTT
AGGTGAATAATTTAATTTAAATGACAAAACCTTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTTCTGATTTAATG
TAGACTTTGACTTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAAATATTTTAAGTACATTTATTTTTGGTGTGTTTATTGT
ATAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAATAAAGTGTGTTGCTACAAC
CCATGATTATTTTCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTCAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCCTCCCTGCCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCTCAGGCTCCCGACCGAAGTTTCTCCAAGTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCATCCCCTGGCCGGTCCGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCACCACTGCTCACGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGG
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGGCCCCGGGTT
CCGGGGTCTCCTTTCACATCCAGATCGGGCTGACCCGCGAGTTTCGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGAGACAGAAAGTTCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTCAAACATGACCCCAAGTCCG
CCAACCTCCTGCAGCTGGTGCGCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGTGTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCAGTGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAAGTGTAGTGGGGCCCGCAAACGGCGCCTGTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTTCTG
CCTCATCGTATACGGGCCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCCAACGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
GGGTGGTTTCAATTACAGCAACAAGGACACGCTGAGAAAGCGGCACCTATTGGCGCCTGGACT
GCAAGTGTATCACGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCCGC
TGTCAGAAATCCTCACGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCTGAGA
AAGTGTGTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCCTCATCACCCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCACTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCTTCATGTACCCGGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCACGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGACG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTTCTCTGAGGTCCTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCCCTGCCCAAACCTGGATGGGACACGTGGGGAGTGGGGTGGGG
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCCAGCAATTAAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACTTTG
ACTCCAACCTTGAATGAACTTTTTTTGTGCATTTTCCAGAAAAACAACCCTTGAATTA
GAATGTTGGGACCACGATACTTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCTGCAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTCTGCCCGACTC
TCTAATGGAAGCTTCAGTGACCATCACTCACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAAATGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAAGTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCCGCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

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FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCTTTCTTGGAGTGGTCGCCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCCTTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATTTCTCCGCATATCTTACCACGAGATTTTCAAAACATTTTCAAGGC
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCATTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTGAGATTCAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTTCAAGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC
TTTGGATTGTGACGCATCATTGGTGAAGAGTCATTTCAGGAGATCTGTGGTAGGAACTCCA
GCATACTTAGCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
CGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG
GAGGTGATCCGCGGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG
CGGCGCGTGGCCACAGACCGCCGCCACTTGGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC
AACCGCCGCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCGGCCCTGGGCCTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

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FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCCAGGCC
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTATC
CCACTGGAGCGAGCCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTGGCCAGGTGACCTTCTGCGATCCTGTCATT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCTTGAGGCGTTTCGAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCCTGCAGCTCCCCGAGCACAAATCAGCCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCCAGTAATTTCTGCCCCAAGAAG
ACCCCTTGGGTGAAGAGATGACACCCCCACCCAAGCCCCCACGCCTCTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAACGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGGACACTTTGGGAAGGTCCTCCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCT
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCCGCTTTGTGACTGAG
TTTGTGCTTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCCGTTCTACGTGGCTTGTGTTGTCTTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGCCGTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTGCGGTGCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTCGTGCCTACCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC
CCACCTGCACCCACAGCCTCCTACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC
TTTGTGTGAGAGCGATTCTTGAACCTGA

SEQ ID NO: 13_AI021023_M PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATCGCAGACTTTGG
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA
GTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT
GCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGG
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTTGTGCTTACCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGAGA
GCGATTCTTGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACACGGGGGCACCACTATCTGCACCAG
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCTTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTTCGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGTCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGCGCACTGGAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCCCTCCATCGT
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAAGTTTGTACGGAGACACAAGCTACCCAGCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTTGGGACTTGACTTT
GGAGAAAAATTGTATAGTCTAAAATCAGAACCTTTGAAACCATTTCTTTACTCTTCCAGAT
GGAGACAGTGCTTCTAGGAGTTTAAATACTAGTGAAAGCAAGGTAGAGTTTAAAGCTCAG
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT
TTTGATGATGTCAAGTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAATAAACTCTTGGAAAGCCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAAGTGAAGTATCCCTCTGGG
CCCAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
TTATTCCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA
CCAACCTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAGCTAACGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGAACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTGGAGCAATCACTGAA
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCATTTGGAAAGGTTTTCTTGTTAGAAAGAAGACCGGTCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAGTTTCGAGACAGAGTTTCGGACA
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAGCAAACTTGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAAGACATCTGTTTTTGCAAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAT
GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTCGCAACAGGGTGGCTCTGGGA
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGGCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGGAGTCCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCTGACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
CCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCCTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTGAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCAGCGGCCTCTCTGCTGACTGAGCTGCTGCAGTTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18 SGK_H

ATGACGGTGAAAACCTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAAACACCCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCCGTCTCCAATCCTCATGCTAAACCATCTGACTTTCACTTC
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTTCTATGCAGTCAAAGTTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTGCGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCCTGGTG
GGCCTTCACTTCTCTTTCCAGACTGCTGACAAATTGTACTTTGTCCTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAACAGAGAATATTTTGCTAGATTACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAAATCCACCTTCTGTGGCAGC
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAAGTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG
TCCCCTGACAGCGTCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCTATGCGCCTCCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19 AA107515_M

CGGGTCGACCCACGCTCCGCCGGTTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT
CCATTTTGA AAAATGTCCCATCCTCAGGAGCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCCTCAACCCCTCACGCCAAACCCT
CCGACTTTTACTTCTTGAAAGTGCATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA
AGAAGAAAGAGGAGAAGCATATTATGTGAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTTCTGGTGGGCCTTCACTTCTCATTCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCACGCCTGAGTATCTGGCTCCTGAGGTCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACCAAATATTACAAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA
CCAAGAGGCTGGGTGCCAAGGATGACTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT
TAATTAAC TGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACCCAAATGTGA
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACGGCCAGTGTGAAGGAAGCAGCAGAAG
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCTCCTCTGAGTGCTCCCGGGAT
GGTTCCTGAAGGACTTCCTCAGCGTTTCCTAAAGTGTTTTTCGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCGCTGCTTGATGGGAGCTTTCGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTTCTTCTTCTTCTTCCCTTCCAACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
ATGCAGGTCTAAGAGGAATCCCCGCAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTTTCTATCGCAGAGTGTTCACT
TTGTGTTTGTGTTGTTTTGTTTTGTTTTGTTTTGTTTTTCCCTTGGCGGATTTCCCGTGTGTGCA
GTGGCGTGAGTGCTATGCCTGATCACAGACGGTTTTTGTGTGTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTTTGTTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTTGTAAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTGAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTTAGAA
AGGGTTTTTATGGACCAATGCCCCAGTTGTGAGTCAAAGCCGTTGGTGTGTTTTTCAATTGTTT
AAAATGTCACCTATAAAAACGGGCATTATTTATGTTTTTTTTTCCCTTTGTTCATATTCTTT
TGCATTCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
GGGTTATAATATGTACAATTCTCCTCCTTACCACACAACCTTTTTTTGTGTGCGATAAAC
CAATTTTGGTGTGCAATAAAATCTTGAAAACCT

SEQ ID NO: 20 AA109508 M

CCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCCTACGCTGCTGAGGT
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA
GAACATTCTCTTGGACTGCCAGGGACACGTGGTGTCTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

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FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACCTAACAAATGGCTTCAACGAGAAG
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCCCAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCCTGCTANGG
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAATCCTCATGCCAAACCACTGACTTTGATTTCTTAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACCTGAAAAGCTTTATTTTGTCTGGATTTTGTTAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTAACAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC
CATATTCTGTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG
ATGATGCATTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAG
TTTGCCATTTCAGAAACCATTTGAGCAAAATAAGTCTATAGATGGGACTGAAACTTCTATTT
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAAATTTATATTCTTGTTTAAATAAGCTTATTTTTTAAACAATTTAAAAGCTATTAT
TCTTAGCATTAACCTATTTTTTAAAGAAACCTTTTTTGTCTATTGACTGTTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTTTAAACAGTCAATTTTCAAGTTCAGCT
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTATCACACCAAAACTAT
GCAATTGGTACATGGTTGTTTAAAGAAGAAACCGTATTTTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGCTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCCTCGCCTGGTCGCCTGATAACTCCCCCGTGCGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTGCTGGGTACCAGAAACACCTGTCTGCTC
TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCCTCGCCTTC
CCCCTGCAGCCTGAGGCCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGAGCCATGGAGGGAGGCGGCGGGCGGCGGCGGCGGCGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCTCCAGCCCGGCCCCGGCCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTCCAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAGTGTTTGGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTTGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCTATCAAGGAGAAGAGGCTCAGCGAGAGGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCCGCCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTGTCTTACCATGCTGTATGGCCAGTTCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGAACCCC
AGCAGCGCCTGGCCGCCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTG
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCCAGGTACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTTCCGTCCC
TCTCTTTCTGATCCAGGCCCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC
CAAACCTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24_SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTTCGCGGAGAGGGGCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTTTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTCCGACAACGTGAACCTGCCCCAG
GGTGTCGCGCACTATCTACACCATCGACGGCAGCCGGAAGGTCAACAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTCTGTAAAGTCGATTACACC
AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAAACCCAAGTTA
GTGACTGTGATTTCGAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCTTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTTCCACCATTC
CGAAGTGAGAACAAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGTCTCCGTCATCATG

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FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTCGGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTCATTTTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAATAAGAAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTCACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCCTCTGGGAAGGTCTCCTTGTTCCTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

SEQ ID NO: 25_W30246_M SGK324_M

ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGGAAGTTTCAGAGGATTGAAGATTTCT
GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCCTGAACTTGACCGTTGCCTGAGC
CCTGAAGGTGTGAATGGAAACGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
ATAGGGAAGGTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCGTGGACAGGTAC
ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTTCTAGTGATGGAACGGTCAAAGGTGGA
GATCTCTTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACTACTTCTGTGGATTCCCACCATTCGGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCACAGCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTAATAATTGTATATAACTGTACT
TGTTCTACTTGCTTGTCTTTAAACAGGGGGCCCCACAGTTCACCTCTCACTGTTAGATTT
TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
CTGGTGGTGA CTCAACGCCGCTTCCCCACCATGGAGGCCTTCCCTCTGCGAGGTGACATCA
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTTCATGGCCACCCTGTG
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

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FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCCTGTGAGCAGGGAAGGAGCTGGTAAGTGGCCATTACTATGTGGCTGTGCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGGAAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTTCGTTATGCC
CAAGATGACTTTGTCTGGATCATAGTCGTGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGCGAAGCCACGG
CCCATGGGCATCATTGCCGCCAATGTGGAAAAGCATTATGAGACTGGCCGGGTTCATTGGG
GATGGGAACTTTGCTGTGCTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAAAAACCTT
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT
CAATGTTAAATGTCACAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCTATCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC
CTGTGAGATTAATAAGGTGCATTG

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ATGCCAACCGCGCCGGTCTGCGCCCGCCGCCGCCAGCGACCCCGCCCGCCGGCA
CCCAGTCGCCCTGCGCCTCCCATTCGCGGCCACCGAGGCCCATGTGACCATTCTCTGAAA
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGGCGTCATGCCGCTGTTACGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCCTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTACCCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCCGCTGGGAACCAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGCGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGTCTCT
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCCTTCCGAAGTCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCTCCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCTTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAAGAAG
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRAK2_H

CTCCGCTGCTGTGCCAGGAGTCACTTCACGAGAAGCCAGGTCACAACCGTCGGCCCTTG
TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTTCGGAGCTCCCTGGCGCCTCGCCCGGCTG
GAGCTAGAGAACTCGTCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCCGGAGCGGTAAAAATAAGTGAATAAAGAAG
CAGACCTGGGAATCACCTAACATGTGCGAGGAGGAGATTTGATTGCCGAAGTATTTAGGC
CTACTAACTACAACCTCCTCAAATTTCAATAAAAAATGGAAAACCTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAAATCATTTTGTATTTGGAATATGCT
GCAGGTGGAGAAATTTTACGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTAATAAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACCTTCGG
GAAATCATGGGAACACCAGAAATTTTAGCTCCAGAAATCCTGAACATATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAAC
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTAATGTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAGTAAAATTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M DRK2_M

CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
GTCGCCGCGGGAGTGCCTCACAGGGGCCTGGCTGACGGCGACCAGCCGTTGTGGGGAA
GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCAAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAATGATGTTATCAGACTCATTAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGGAAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCCAGAGAAAAGACCAACAG
CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA
AGACCTCCAAGTCCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGT'TTCTAAAAGATTTTCGATTTCGATGACTCCTTGCCAGCCCC
ATGAACTTGTTCCAGATTTGTTCTGTTAGCATTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTCCTGTGTGAAATTCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACAACACATGGGAGTGTTCAGTGTGTGTCGGTGGTCAATATCTATGTTTCAGTCCTGATGG

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FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCAGTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAGAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCCTTAGATAACTTTAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTC

SEQ ID NO: 31_H01248_H, DRK1_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
GGCCGGGCAGGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCCGCCGCCGCCAGGCCCGC
GGGCTGCTGACAGAGATACGCGCCGTGGTGCACCCAGCCCTTCCAGGACGGCTACAGC
CTGTGCCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCCTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCCTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCCGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32_AA021445_H

CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGGCCGCCGGCCGCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCGCTGCCGTGTCCCTGCGGCCGGCCAGCCGCGTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTGTCACTGTCCGAACATTGTTTCATCGTGATTTAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCAAAGTGGACATCTGGAGCCTTGG
AGTTGTCCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCGCTGCTGAGTGGAAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

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FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCTTGCCTCTCGGAGCACTTCCTAGCATGCCCCGAGCCCTGGCCTTTCAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGCGCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCTGTCAGGTGGCCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAAGTGCATGCCAGCAGCTGCTGAAGCGCCACCGGG
ACCTCTCCGCTTGTCAACATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACACTGGCCATGACCAACCTACAGCTGAGATCCCACCGGACCTACAACGGCA
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTACAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTACAGCCTTCAAGCCCACCCCCAACCCACCCCAACAACCATCTCTT
CAGGCAGCCAGTAATAGTCTTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCACTCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCAACATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTC
CAAGCAGCTGAGTGCTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTTCGGACCAGTCCCGGGGTTC
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA
TACCACGTGCGCACTACAGCAGGCCCTGCTGTCTCCCACGCCGCCAGACTATACAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCTGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGACACAGCTCATTTAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCTTACCCACCCCGCCCCACGG
GTATGCTCACACAGCCGGCACTGATGCATTACAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACTGCTGCATT
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTATAGGGAACTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCTC
CGTCCATGAGCACACAGGCCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCCGATGTGCGATGCAGTTCTCAGTCAGTCTTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCAGCA
CCTGAGTGATGGCAGCCAGCATTTAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTACGCATGGAGCAGGCAGGCGTGTA

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FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTTCCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H

CTGGGCGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTCTTCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACCTTCTCCCAAGTGAAGCTT
GGGATTCACTCCCTAACCAGAAAGAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACTTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAAAAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTACGACAGTAAGCAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTCTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTGCAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGTCTGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTCAAGGACAACCTTGAGTGGAGACATTTTTGTAAATTTTAAAT
AACTTAAATTTGAGATATGCAAAAAA

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ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCAACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCTTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGCAGAGAAGTGTTTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTTCAGAAATGGCAAAGAAAACAGCACTATTCTTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT
CCTGCCTCTCCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTCAAACCTCACAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTCACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

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AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTGGCCGGAACCTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTCGCTATTAAG
ATCATTGATAAGACCCAGCTGAACCCCAAGTAGCTTGCAAGAGCTGTTCAAGAGAAGTCCGA
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTGTAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC
GTGCACTACTGTCATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCTATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCCCTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACTCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCTTGTGGCCAAATGGCAA
GAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCACGAGGCCGCACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGACCTGAGGTCACAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

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GTAGCCGGCTTGGCGTGACCGTCCGCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTGGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTGCTTTCTCAGCCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTTACCTCTGCTTCCGGCCCCCTGTGTGCAACCCTAACAAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTTGGAGCCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTGATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTGAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGGCCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTGCTGCTTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTACCCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTCTGCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACCAAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTTACAGCCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGCGAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAACGACCGAGA

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FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACGAGCCCT
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCTTGGAAAGCAGTGGAGGCCCAGGAGGTTGA
TGTGAATTCGTTTTCTGGAACCTCAAGGAACCTTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCCTTGAGGTTTGTGTTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCCCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCTGTTCCTTGCCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAACCTGGAGGGGTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCAGGCTGGATGAGCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTGACAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCCGCTACTTGGAAAGGGGAAAATTATTTTATACTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTT
TTCCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGATGAGCCCTGGCGAGTTTCATCTTTTCGACAACCTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACCTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTACCCC
TGTAACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGACGTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTTACAGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

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FIGURE 2BB

TGACTTCTGCTTCTAGATTCCATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTTGTGTTGTTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACCTTTGGCTGGCCTGGAACCTCACTATGTAGACCAGGTAGACCTTAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCAACCATGCCCA
GTTCTTCCTGGTTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

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GGCACGAGGCGCGCCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCCTCCCGCCCGCCCGCG
CTCCTGTCCGCGGTGTCTAGCAGCGGGGCCAGCATGGTTCATGGCGGATGGCCCGAGGCA
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCAGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTCCTGGCAAATCCTGTCTGC
TGTTGATTATTGTTCATGGTTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTTCGGTTTTTGAAATTTCTTTAAAG
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTGAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCCTTTTCATTTCCAGCATCTGGCTGTGAGCGGA
AGCTGCATTTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGGTGCAGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCGGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTTCAGTCCACACGCGAGCGGGCAGAGACGGCACACTCTGTGAGAAGTGAC
CAATCAACTGGTTCGTGATGCCTGGGGCAGGGAAAAATTTCTCCATGAATGACAGCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGACAGTTGTTGTATGAACAAATAGGACCCGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCT
TCTGTCAAAGGCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

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FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTTCAG
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCTCCGAGCAGATGCAATACAGCCC
TTTCTCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTGAGGTGAAGGAAGAGTGTATGTTCCCTATTTTATTTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCCTCGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCCCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCTTATTTTTTCACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTTGAC
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTTCATAAGCAAACAGCTGTATAAACAAGCCCCCA
TTTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCACAACCTTATTCTCCACTCAACA
GCCGCTGGCTTTGGGGAAGAGGCCGCTTTCAGGTGACAGTGACAGCTGTCCAGGTGGCCG
TGCACTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCTGCCTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCTACAGAACACCCCCCTTCTCAATTGCCAAGGGGCCGCATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCAACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCAGATGGAATAATGTCACATTCCCAGTGACAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCAACAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGGTTTGTCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTTAATTACTAAGAAAAAAATTTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAAATCAAAAGTATAAATTGTC
ACTTAATGTTAGAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTTCCAACCCTCT
TGA

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FIGURE 2DD

SEQ ID NO: 39_AA207220_H

GCTGTGGCTCCCCGTCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCAAGCCCCAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCCAACCGCCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCAGACAGCCTTGGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCTTGAACGGCTCCAGAG
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTCAGGCTCTCAGATGCAGCTGG
TTGCACCCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGCGGCGGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCGCGGCGGCCTGCGAGGGAAGTTTCCTGCCTGCCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCCGAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTTGGTTTGGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTT
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTTACGGTGGAGCCTTTTCAAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGCCCCGGAAGCACTGGCATCCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGCGC
TCCTTCGAGTCTGTGGATCGCGACGACCAGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACCTCTGGTC
TCTTTTGTCTACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGGTTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG
AACCTTGCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41_Z36720_H

ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA
GATGTACACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCTG
CACAGGCTGGAGGCCTCCCGGGCACCGGGCCCGGGCGGGGCTGATGGGGTTCCCCACATT
GACACCCAGGCTGGGTGGCCCGAGGTCTTGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT
GTGCTGAGCACCAGTGGGGTGCACTGTATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCACTGGTCTCACCGGGCCAGGGAGATGGTGTTCTTGCCCCAGCC
CAGGCATTCCCTGGCCACCTGCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGTTT
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGCGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCCT
GGGACTGAGCCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGGCAAAGCCCAGGGGCGGGAAACCTTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCTTTGTCTATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCCTGTTTACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCTTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTTCCCGGTGCTGGTCAAAGAGAAGAGCTGCAGAAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

SEQ ID NO: 42 SGK088_H

GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCCACTGACGTGGAGGTGGATTGG
CTGTGCCGTGGCCGCCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC
CGAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGGCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGC GGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTGAGTGTGTTAACACC
CATGGCCAGGCCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
CTGGAGCGGCTGTCCATTCCCGACTTCCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGACTCCCTGACGTACACA
GTGCAGCACCAGGTGCTGGGCTCGGACCAGTGGACGGCACTGGTCAAGGCCTGCGGGAG
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCAGC
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCAACCTTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGGCCAGGTGCTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

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FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCAACGGCACACAGACCTGCTCGGTACACATTGGAGCTG
GCAGAGGCCCCCTCGGTTTGTAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAAACT
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGGTCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTCAGCTCAGACAGCTATG
GAGGTGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCTACTTGCGGCGCATAGTGGAGCGT
AGCTCCGGCCTGGAGTTTTCGGGCCAAGTTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCCTTCGAGAGGCGCCGGGACTGGTCAATTGTCACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTGTCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCCGGGCTTCTCATCAAAGTGTTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCAG
ATCAGCTACAAATGCCACCTGGTGTGTCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCCAGAAGGCCACCCCCCAGTGGGGGGCTCTCATCTCC
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC
GAGTTCTCTGGCTCCCGGGTGTCCCTCACAGACATTCCCAGTGGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCAGCCCAGAGGCCCTCCCTCCCGAGGCCAGGAGCCCCGAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGAGGGGCGAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGGAGCCCCGGCCGGGAGCCACCCGCTGGCCCGGGGAGGCCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGGCGCTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCCTCAGCGAGGCGAGCGCCCCACCAGCCCCCACTCGAG
AACCAGGGGCTGAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
GCTCCGAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA
CCAGTCCGAGCCTCCAAGCCTGCACCACCCCCCAGGCCCTGCAAACCTAGCGCTGCCC
CTCACACCCTATGCTCAGATCATTCAGTCCCTCCAGCTGTCAGGCCACGCCCAGGGCCCC
TCGCAGGGCCCTGCCGCGCCGCTTCAGAGCCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
GTGGCCTCCCCACCTCCGGGAGCCCCGAGAAGCGCGTGCCTCAGCCGGGGGTCCCCCG
GTGCTAGCCGAGAAAGCCCGAGTTCCACGGTGCCCCCAGGCCAGGCAGCAGTCTCAGT
AGCAGCATCGAAAACCTTGGAGTCGGAGGCCGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC
GAGTCGCCCCCTGTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGGC
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCCGGCGGGGACCCCCG
CTGGAGCTGGTGCAGCGGCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGCGA
GAGCCTGGCCTCGTCCGCCGCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGTGCGCATGCGCAGGCGGCTGAGCTTACCCTG

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FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCG
GGCCGCAGCACGCCGCTGTTCCGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGGCCAGCGCCACGTTCGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTCAACAGTACGTGCGCAGTGAGTCAGAC
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCCTTGAGGTGAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCGAGTCCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAAGCCGGGA
GACAGCCGGGCACCTTGACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTACGCCCC
TCATCTCCCCCACAACCTCCTAGCCAGGCCTTGTCCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCCTGCAGGCTGCCCGGCCAGCGGAGCCACC
CTACCCAGTACCCACGTACCCCAAGTGAGCCCAAGCCTTTCGTCTTGACACTGGGACC
CCGATCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGTCTTCTCTACTCCTGTGTAT
GTGGTGACTTCCTTTGTGTCTGCACCACCAGCCCCTGAGCCCCAGCCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCTACACCTTCTGAGGAGAAAGCCAGGGGCCGCTTTGGTGTTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCTGGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTGACAGGAGTACGAGGTGTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGACGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT
GTGGACTTTGGCAGTGCCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC
ACGGGCACGCTGGAGTTTCATGGCTCCGGAGATGGTGAAGGGAGAACCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCTCTTCTTGCGAAAGGTTCTCTCTGTA
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCAACCACCAACCGGCTCAAGGAGTTC
CTGGGCGAGCAGCGGCGGCGCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC
TCCTACCCTGGCGGGCCCCTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG
TTCCACCAATGCCACGGGACATTCCAGGGCCACGCTGAGCCAGGCGGGCCTGGGGCTT
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
GACCCCAAGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTCAGGGCAGTAGGCTGGGAGTCAAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTCAGCATCCCTCAGAGGAGAAATGTG

FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43_AA542015_M SGK088_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTCTGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCCTGGGCGAGCAGCGGCGACGTGCGGCTGAGGCTGCTACCCGTACAAGGTGCTGCTC
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
TAGGCTGGAGTGGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCCAGGGATGTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTGTAT
TTATTTATTTATTGCCTTTTGTGGAGTTTCCTTTCTATCCAGTCCCTAGTGCCTATGTTG
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTGTCACA
AGGAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44_R19772_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCCTCAAGCGAGAATGGAGGC
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACTTCATCCACAGTTCC
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCCTGTGCGTCGG
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTTCGCGATGGTCCG
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
CTCCCACCACCTATGAAGATTTTTTGACAACGACCCTACACAGGATGAAATGTCCTCCTCT
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATACCGGGGGAGCTTG
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGGAAAT
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGCGGAACTGGAAAAGTGTATC
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCCTCATCAAG
CCCATTCAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTGAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGGCGCGTGTTCCTCTTCGAGCAGATTGTTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAAGGAGCATCAAGATGAAT
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACCTCATGAACAGA
GAGACTTCTGAGAGGGTGTTCCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCCCCGCCGCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTCACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTCATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGAGAAACACGGGTAAA
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTTAAA
GAGACGAACAGTTCCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTTTCATCCAAGAAGTGGCCCCAGAATTCCCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCCCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAAACTGCACT
ATTTCTGGTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTTCTTGGAAGGAAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAAGT
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAAGTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC
CTGCTGGGGAACCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCC
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTCATCAATGTGATCTTA
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGACATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA
GAACGTCGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTGTCTCGCGCGGCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCGGGCCCCGGCTTTGTTCTGTCGGAAGTGTAGTGGTGAGA

FIGURE 2KK

AAAACCTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTACCATCAACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCCTCAAA
CAGTGGAAACATTTTTAAAGTTGCTTTTGTGTGCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCGGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTTTGGTGGTGGAAATGTCACAGACA
TCAAGCATTTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTCGGGGCACTTTACAGAAGGAAAAGTTCTTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTTGAAGAATATTGGGAAAAGGG
AGCTTTTGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAAA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAACACATGAACACATCATACTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATTCTGGAT
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTGGCA
AGCTCAGAAGCGAAGCTTTTGTAGTTAATAAGAAAAGGAGAACTACATTTTGAAGATGCA
GTCTGGAATTCCATAAGTGACTGTGCTAAAAGTGTTTGAACAACTTATGAAAGTAGAT
CCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA
GAAAGTGTTGAGGAAAACACAACAGAAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCCTGGGGAAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTCTGCAACCAGTAAGGACAACCTTTGAT
ATGTGCAGTTCAAGTTTCACATCTAGCAAACCTCTTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTTGGACAGTACAAAAA
CAAAGCTGCTCTTGTAGTACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGACACAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATTCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAACAAGAGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTACATGTGTTCTGTGAGATTTTAGGTT
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG
CTTGCCATTAACTTGCTGCTAAATTCCCAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCGCCCTCACAGGCCCTCCTCACTCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCTGCCGGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCAG
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTTCGGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGAAGGAC

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FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTTGCGGCTGGGCAAGCAGATCTTGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCAACAAGAACCGGGAGATGGGCGGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACC GGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCCTGGACCACATTTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG
ATCATGTCAGTGTTTGAAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA
GCAGAACACCCGGCAGACCGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG
GGACCTGCTCCGGGAGAACACCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCCACCCCGGGGGTCTTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTCACCCCGATTCCCAGCCTTGTGCCCTTGCCCTGTTCTCCTAAGCACCTGT
CCCCCGCAATCTCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCCTCCCCGGCACTAGCC
TCGCTGTGTCTTCCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCGCGCCGCGCCGCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGAGTCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTTAAATGGAAACCACCCTTGG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTCACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCATTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTGCTTTCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC
TTGGCTCGACAATTTACCAATTCTGTGGTGACGTCAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG
GATTATTTTACAAAACCAGACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC
CTAACAACCACCACTACTTCTACCACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAAAAACAAGATAAAGCTTGGAAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCTG

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
ATTCACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAA
TAAGAAATCCTTGCATTTTTTGTAACACTGAGTCTATTTCAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACCTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCAATTCACTTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGGTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATTCTTTGAGATGACTGTTTTTGATTTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTTCCTTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCACCACCCAGCC
CAGTTTAGCAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAAGGTTCTTCCAGGGCTGT
ATTTCTGCAGTTTCGGTTTTTCATTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTCATT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTATATACATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA
TGCTTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGT
TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

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FIGURE 2NN

TGAAAATTAAAGATGCCTTCTAGAAATTGGTTTGCTCTGATCATTGCTGATTCCCTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50 AA061797 M

GAAATAAGCCCTGCGGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
 CATCGAGGTGTTTCAGAAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC
 ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
 GCTATGGCAAACCCTTCAAGCCCTTAACCTTCTGTCAACAAGCACAATTGTATTTCATCGGGA
 TGTA AACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
 ATTTGCACGAATTCTAATTCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
 CCGAGCCCCCGAACTTCTCGTGAGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGG
 CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAATCCCG
 CGTGGAACAGCTTTACCTGATCATCAGGACGTTGGGGGAAGCTGATTCCAAGACACCAGTC
 TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
 GACTCTTGAAGAAAAATTCTCAAATGTTTACGCTGTGGCTTTAAGTTTTCATGAAGGGATG
 CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCCAGCTGCTGGACAGTGCCTACTT
 TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCCGAGTGAGGGGAGAAGCCGAAG
 GCGCCAGCAGAATCAACTGCTGCCTCTTATTCTGGAAGCCACATCTCCCCCACACCTGA
 TGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCCAAACATTTAGGGGACTCA
 TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
 TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
 CTGTGCTTTTTTCCACGCCAGCTCCATCTCCTAAACATTCTCTTTAAATGTTGCAGTATC
 AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTACCAGAGCCGGGCTTCTCAGGCAA
 TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAAGATTTCCACGTAGCCGT
 CTCACCTCAGCCGACCAGTGGTGTCTGAAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
 GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
 TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
 TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
 CGAACTAGAGAAAATTCCAAACGTGACCAGTTAGTGACAGACTACAAGGAATCGACCAC
 CATACCACAGTAACGCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT
 CACCATGGTTTCTCTTTCTTTTCTTCTTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC
 AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAGACAAGCAGGAGGCCAGCCTAAG
 CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAGTCCCT
 GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCATTG
 TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG
 AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
 TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
 GGGCCATAACTGAACCTGTGGAGTTCTTGCCTGTGTGCAGGAAACCCCTCTGGTTTTGTCT
 CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
 GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
 TCCGTGTTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
 ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
 CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTTAGTTTAGAAT
 GCATTAATGTATGTAGAAGCTGGGCTATTTTCAATTATTTGAAATTGTAGCTATTGTTAA
 TTAGCACTTAATAACTAAGTAGCATTATGGTAGTCTAAACTATTAGAGTTTACTACAAAG
 AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
 GAAAGCTATATAAAGATTAAACATTTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG
 TTCTTTAAATTATTTTAATAAAAAGCCAGAAACATT

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FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAACCT
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCGAAGCA
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAAGTTCAAAGCGTTCGAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT
CATCGAAAAAGGGAACACCCAAAAGTTACAAAACAGTGGACAGCCCCAAAACGGGAGATCC
AGGAGCCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAAGAAAAGTCTTGGAAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGACAGAGA
TCTGTCACTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCCAGTCCCTATGGTGAAGGCGGTCCAGCAGCCCTTTCTGAGCAAGCGG
TCTCTGAGTTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCTT
GCATATTCAAGACATTCTCTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCCAGTATCTCACCTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTCACCTGTATTTTTGCCTAGAAAAGAGAAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAAACACATCTAAACACAGAGGTAAAAAATTTCTTCAGATACAGGGAAA
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCACCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCTCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCCTCTCAGGCAAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAAACAGCTGCTATTCCA
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCTCCACCCCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAACTCTTCCTTCAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACTTACTCACAGACCTTCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCCAGACTCTCCAGAACCAAAGGCAATCACACCACCTCAGCAACCATATAAAAAG
AGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGGCTTCCCAATCACAGCCATTCTGTGAAATCAAATCCTTTCGTGAG
TTAATCCACCGAAGTGTTGTTAACATGAAGGAAATTGTCACAGATAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGATTTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAATCTGGTTTGGTGCACCTTTCTGAGGACCATATCAAGTCGTTTCATG
AAACAGCTAATGGAAGGATTGGAATACTGTCAAAAAAGAATTTCTTGCATCGGGATATT
AAGTGTCTAACATTTTGTGCTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAATACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAACATTTCACAAAGAAGCCTATTTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

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FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACACCCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGGCCCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCCT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAAGTTTCCAGGGGAC
CAGGACCTCCGTTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTTCGGGCAACCATT
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAAAATAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAATCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCCTTACTAA

SEQ ID NO: 52_AA789239_H

TGAAATGGAGATGTATGAAACCCTTGAAAAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT
TTGAATTTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTTCATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCCTAGTAGTTCTGATTTGGATTTACTCCATAAAAATTGTTTTGA
AAGTGNGATTTCATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG
TTTATACCAATACACTGCTAAGTAGTTTCAGTTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCACAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTT
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTGAACCACCAAACCCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCCTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTCACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

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FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTCACAAATATTTGCT
CTCAGCTAACTATCAGGCTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATAACAAGATGACAACCTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTTCGCTCACGATTACTTTACTAGAGATGGATTTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACACCAGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
ACTGAAAGAACAAGAGACGCACCTTCTTCAAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTGAGAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTTGGTTTTTGCTAGCAAAATTTTCAAAATTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCATATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCTAGGTTAAACTCCTTGAGATGAAACTATTTCCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTTCCTTCCATTTAGCCAGAAGAATTTCCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
GGTGGTCGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACCTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAAGTGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGACCTGCTGGGCCAGTTCCCTCCTCTACCCTCCACGACAG

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FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCCTTCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTGCTTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTTCATCCAGCAGAGAAAGAGACTCACGTCCTACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTCAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTCAGGTACT
CAGAAGGGGCCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCCACATGTGCGGTGGGTGAGTCAGTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCTTGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTTCGGGAGATG
CGGCATTCCAAAAGAACTCACTGTCTTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTGAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAACACTACTGGGACTTAGTACTTACGATTTTCATTAAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTTCACAGTCTTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTTCAGAAAACAAGAAAACGCAAGTATTTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTTGTGATGATGAAGAACATGAGAACTGTTTGACCTG
GTTTCGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTGAGTCAACTAAACATTCTAATATTTTGT
AAACATTAATTTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT
AATTAACCTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT
TCTTTTGAATTAACATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGTAGTAAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

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FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAACCAAACCTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTGTATTCTTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGCGTCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGTTTCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCCTGAGTACCGCAGCCGCTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCCGGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCCAGAGCCGACCCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCGTGCAGCCAAGAACG
TTCCAGGCAGAACTCCGCTCCCCTGCTCCAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACAGGCCCTGATCC
GGGGTGACTGGAACCGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGGAGGCCCGGCCCGGAGGATGTTTCAGCACCTCTGCCTTGCCAGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGAGGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTACCTGGCCCTCTGTTCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

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FIGURE 2TT

TCAGAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTTCAC
AGAAATGGAATATTTACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCTT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCCCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAACCTGCCAAACTAAAGCTTTCCGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGCTG
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAAATGAAAAGAAAATTTTAT
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTACAAACTCGGC
TTCTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACCTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCAACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACGAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTTCAGATGATTGGGCTGAC
TTGGATGACTTGGATTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGGAGAGTGTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCCACCTAATCCATGGTCT
AGTTCTGGCTTGCTGGAAAATCTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCAGACCCTTCC
CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCAGGCCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAAGCTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATGACTTTGGGCTGGCTAGAAGATAACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTGGTACTCCGGAGTTCTGCCCCAGAAGTTGTTAACTAT
GAGTTTGTGTCACTTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTTCGGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTTCGCTCAGATCC
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTTCTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAGAAAGAAAGAAAGGGGGAAGAAAGGAAAGGCAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTGTAGGTGAAAGTGTTTTTATTAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAACTTGTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
TGTCCGGGGTGGACGCATTCGGGTAGCCGAAGAAGTCCAGGATTGCCGAAGAAGTCCCA
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGGCCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGTTCGCTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGCTCCTCCGCTGTGCGCCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGGTCTCTCCAACCTTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTTCAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT
GAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATAACATGGGTGTGGCATTGAACCACATAATGAGAAATATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCAGTGTTTTTTTTTTGTTGTTGTTGTTGTACATGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTTCGAGCAGCTGGTGCTGGTGGACCAC
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTCT
ATCTTCATCACAGAGTACGTGTATCAGGCAGCCTCAAGCAATTCTTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTTCAGCACACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACCTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTCAAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCCCTGCCCGCCGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCACTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACCTTTGCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCTCTCCACGAG
GACGACCGGATGAAGCTGGCCGCTTCTTGGAGAGCACCTTCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCCTCTCCTGAGAGTGGGGCTGACCTGCCTTGGGCGC
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCCTTAGGATCAGG
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCCTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCAGGGAAGTCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGACGAAAGCCCCCT
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCTGAGACCAG
AACTTGCAGCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCTCCAATGGGCTTTTTT
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAAACCTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA
CATAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCCGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCCTTGGCTCTTGGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCACTGTGTGTCACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCAGTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAGCCAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATCTCACGCCTTCCAACCTAAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCTCATGCTAAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAACTGAACTTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M

CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCGCCGACCCTCAGCCACAACT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGC GGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCAAAGGCCAAAACCTCCAACGCCAGAACCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCAGGACCTCGCTGCTGAACTAGTGCAATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCCTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCTT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTGAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCCTGCTCA
GACCAGTCTGATCCCTTGACAGACCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCTCCTCCCAAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCTCCCTGGGGAAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCTGATGAACGCTTCCCCTCAGAGCCACCTGGTTTCCTTGG
TTCTTGAACCTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACACAGAGAGAGAGAGAGATTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

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FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCGAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCGGCTCCTGCCCCCAAGA
ACGGCTCCAGCTCCGATTCTCTCCGTGGGGGAGAACTGGGAGCCGCGGCCCGCCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGCCGCGACCACTACCACCACTGAGCACCGCTTCTTCCGCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCTTCTCTTTCCCTGCCCCAGCCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCCAGCAGCCTCCAGCCGCTGCCGCCCCCTGGGGAACAGG
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCGCCGCGGAGAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTCTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCTTGGTGTGAAGTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCCT
GGGAATCCACAGTAAAGGAAAGAGTGCATTGTTTTGGTGAAGTGAAGTATGACGTCTG
GAACACTTAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG
ATTTAGAGAGAGATGTCCAGAAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAACAAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCTCAANNATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCCTCCTCAACAGA
CAGTGCAGTATTCACTTTCACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCTTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGTCAGAGCCAGTTGTCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTTCAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2YY

GGCATTACCGAAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGATCGTTTGTGGATC
AAGTGCAGAGAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCTTACCAGTTCTTTAACTCAAGTTGTTTATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG
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TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCCAAGTCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT
TGGCTTTCTCCCTCTCTGCACCATCTTCTCTTCTCTCTCTGGAGCAGGAGTGTCTAGTT
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTTCATTCCATCAGTGATAGCTTCTACTC
CTATTCTTCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA
TCCCACCTTGGTACAGCCTGTTGCCAATGTGCTGTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCTGAGTAGATT
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC
GGTCTCTGTTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCAACTACTGCTGTTGCACCAA
GCAAACCTCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCCTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCCAAGTCA
CTACTACATCAGGAGTGAAACCTGGAAGTGTCTCCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCAGTCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTTCTCAAG
TCAAAGAAGGCCCTGTCTAGCAACTAGTTTCAGGAGCTGGTGTCTTTTAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTTCAATTTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGGCCACAAAACCTACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTTCAGGTGACAACTACAGCAAACAAAGTGGGTCTGTTCTCTG
TATCAAAAACCTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTACAGAGCCTTACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCTTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTACAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCAGCAGACCCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA
GTGATGGTGGCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTAAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGATGAAATTCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTTCAGTTTTTTATCCA
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACCTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTCTTCTGTGTGCCATCTTAGTG
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTGTGTTCTACCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTTCATTTGTCTCTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACCTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTAGAAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCCGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAATAACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTAAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCTGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGT
CCACCCAGCATTTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCTGTGAAGCCCCCTCCCTCCTTTATTATTACAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTCCCCCTCCCCCTCTCTCCTCCCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCTGGGCTTCTCAGCAGCCGCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGGCTCCCCGCCAGCCTGTGTGGAAGGAGGCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGGCGGGGAGAGAAAGGTGGTGCTGCAGTG
GTGGCCCTGGGGGGGCCATTGATTGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
AAACGCTGGTGACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCC
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTCAGGGCAAT
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAGTGCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTACAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT
GAAGTGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCCCTGCCCTTCCCCTCTCTTCTCCTCCCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCTGGGCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCGGGGGGGGCATTGCAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

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FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGCAGTCCTCGCCTCGGCTG
CCCCGGCGGGCCGACAGTGGAGTCTCACACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCTGCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCTCCACCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCATTTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCCAAC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCCAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAAATC
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTTCGGAGGATGAGAAC
TGACGCTGGTTCGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCGCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
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CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCGGAGGGGGAAGTGTGCGCAGC
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGGCACTGGACAGAAACA
GCCATCCAAGTGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTGCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAAGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTCTGGGAAAGAAGGTGGAAGAGCGA
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGGAATAATTTGAAGCATATTATCACCCCTTGCCAGGTTCATCCACAAACGGTGTGAAGAGA
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTTCAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC
GCATGCCTGTTTCAACCATAAGCCAAGGAGCGTCCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAAC TAGAAGTCATCAGTTTACTGGGAC

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FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAATGCCCCTCATTTCATTTCATTCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACTAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGAAAGGAAGTGGATGACACAT
TCTGTTAAGTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAAATATGCCACCTCCCTTAGGACCCCTTCCCTCTGCTCATTGACTCT
TTTGTCTTCTTCCCTCTCGGGGGTGAGGTGAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATAACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGACTCCGCCCTCAATTCTCCATTGTTCATGGAGTACTGTGAACT
CGGGACCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCCTGGGGGAGCCCGAGGCCTATACCGGCTACACCATTGAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACCTTCCCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
AGGATTTGAGTTGAGGAAAACACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC
AGACAGAGTCAAATCTACAGCATATCTCTCACCTCAGGAACTGGAAGATGTATTTTATCA
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCCTCTGGGAAATCGCCACTGG
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGTATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT
ATCCTTCCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT
AGAAAACGATTCCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGACTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG
GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGGCGGGGCGGCCT
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCGCACTGAGGCTGGGGG
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCGTTGCCATGAACCGCGGACACCCCGGCCC
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAACTGGG
ACATGACTGGGTACGGCTCCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCTGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG
GGGCCACTGTGCGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCCGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCCTACGAATGCTTCCAGCACAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT
ACATTGCCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAGCCTAGGTC
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT
ACAGAGTCAAGGTCATCGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTTCTGGGTTGGCCGT
TATATCCAGGAGATTCGGAGTATGATCAGATTGCGGTATATTTACAAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCCTGAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC
AGCCTGCACTATTGACCGGTCATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCCACGTGATGCGGCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTCACTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
CCCGGGAACGGCAGCGGCAGACAATTGTCAATTCCCGACACTCCCAGCCCCACGGTCAGCG
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA
CTGTCTCCAAGCAAAGAAAAACGTCAATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCAACACTCGTCCTCTACAAGTCCAAGTCTCCTCCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCCTGCCCTCGCCCAACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAGTGAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTTCGAGAGTACCCGTGGGAGCGTCGCG
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCGGACCCCCAACTGGCGCCT
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA
GGATGCGGGGCCCGCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTC
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGCAACAGAAAATCCAATACTATTCACTCAGATGGCATCAGTGACTCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTTCAAGATTGCTTGAATACAGTAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACCTT
CGACAGTACGTGGCCCTAAAAATGGTGCGCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
AGCATAGACCTTTATGAGCTGATTAAAAAAATAAGTTTTCAGGGTTTTAGCGTCCAGTTG
GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT
ATTCACCTGCGATCTGAAGCCAGAAAACATTCTCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTTCAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
ATATGGAGTTTTTCGCTGCATCCTTGCAGAACTTTTAACAGGACAGCCTCTCTTCCCTGGA
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATAACCCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTTCGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTTTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCAGCTCAAGCATTAAAGACACCCTTGGATTAGCAAGTCTGTCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA
GAGATATGCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAATGGA
AAAAATGCAAGCCCATTGGTGGATGTTTTTGTAGAGTAGACTTTTTTTTAAACAAGACAA
AACATTTTTATATGATTATAAAAGAATTCTTCAAGGGCTAATTACCTAACCAAGCTTGTAT
TGCCCATCTGGAATATGCATTAAATGACTTTTTTATAGGTCA

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FIGURE 2FFF

SEQ ID NO: 70_AA589241_M DYRK3_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG
CCAAGTACTTTTATTAACCTCAAAGGCTTGCCTCGATACTGCTCCGTATCTACCCAGACGG
ACGGGAGGGTGGTGCTTCTCGGGGGTCGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCCGCTCACCCCGGCTCAAGCATTAAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCGAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTCAC
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCAGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTGAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAACGTGAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACCTTGGA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAAATGGGTCCATTCCCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCTTGA
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTTGAGTGCATCTAATGTCTTGGTGGA
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAATGCCTCTAGTGGAACAAAGTCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCGCGAGGATCAA
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCAGTCCTTCCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTACCCGGGATTTGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACCTTAAGTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCTTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
CAGAGATCCCCTTCCGCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCACAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT
CTTCTCGCAGCGCATCTCCCCTGCCATCGATTACCTATGACAGCGACATACTGAAGGG
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
CTTTAAAGACATGGAGCTGTTTCAAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACA
AATATATGAGCACAACGAAGCTGCCCTATTATGAGACCACAGCGGGATGCTGGTGATGCT
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT
AAAACGATACTGCATAGAACGTGTGTTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA
AGAAGTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCCAC
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATAACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGGAAAGCTAAATTTTGAATCTGTCTTTGTCTTCTAATAGTCT
GTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAT
AAATTTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTLAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCAGAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACCTTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTGT
GAGTGTGCTAGCCCCGGAGAAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACCTGTGAAGCAGCTGCTGTACGCCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT
GTGGCTGCGCCGCCGCCATCGACTTTCCCGCCGAGGGCCCGGACCCCGAATATGACGAA
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAAGCTACTTTGCCAGACGTTTATCAAA
ATGGGGCTGTTGTCTTCTTTCACTTGTTAGTGACGAGTTTAGCTCATTGAGACTACATCAC
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTCGTCAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATACAAGGTGAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAAATCCTGATT
AAGGGTGCAACTAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCCACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTGTGTCTGCCAGTTCAATTGTGGAA
CAGCAGCTGCCACTCAGGCGTAATTTCCACCTAGAGGAGAGTTTCACATCCACCGAAGAA
TCTTCCGAAGAAAATGTCAACTTTTTTGGGTGACAGAGGCACAGTACCACCTGATGCTG
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCCTTATGTTATGGCCAATGTTGCAACA
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA
GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGTTTACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTGT
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAGTTCTAACAGGTTTA
AGAAGTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGAGT
GAACTTTTCCAAAATTCTGGAAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H

CACAAGAGCCCTTCTGTCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
AACCACCTTACAGGCCGGAAGTGTCCGGGGTGGACGCATTCCGGGTAGCCGAAGAAGTCCCA
GGATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAG
AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACCCGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGC
TCCTCCGCTGTGCGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAAGTCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTGTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAAGTATAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTTTAAGTGATGTGATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTGAACACAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTCCTTTTAAGTTTATACCGCTAAACAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAGGCACAGGTAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTTGTAACTCCAATCAACAAACA
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCTGTTGGGTATTGGGTACTTGGCACCCT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCTTTTGTAAAGAT
ATTTATTTTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCTATCACACACTCTC
AGTTTTGGTATTTTGTGTTTTTGTGTTTCATTCTCATCTCAAAGTATTTTCTAATTTCCCTTG
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAAA
TGTTCCAATTTTTCTTTTGTATTGTCAGCTTCATTCCATTGTGTTTCAAGATGATACAG
TCAGTGCCTGTTCTTATGAAGCAAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACCCACAGTCAGCATGCCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAAACTTCCCTTCTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT
CCAAGACGTACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTCAAGGAACCTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGGTGTACTATAAGGCTAGTA
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAATCCCTAGT

SEQ ID NO: 75_AA013524_M

CTGGTGCAGCAGGGCGCCGAGGCGCGCGTTTTCCGTGGCCGCTTCCAGGGCCGCGCGGCC
GTGGTGAAGCACCGCTTCCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC
CGTCGGCGGACGGTGCAGGAGGCGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT
GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTCACGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCCCTGGCGCAGCTG
CACATCGTGTCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGAGCTGT
GGTGAAGTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTAAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACCT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H

ATGGCGGGGAAGTGTGGGGCCCGCGCGCTGTGCGGCACACGCTGCTGTTTCGACCTG
CCGCCCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC
TGGCGCGGCCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTATATTGAAAAG
TATGTAGACCAAGGTAAAGTGAACAAGAGAATTACTTTGGTCCTGGGCACAGAAAAAC
AAGACCATCGGTGACCTTTTACAGGTCCTCCAGGAGATGGGACATCGTCGAGCTATTCAT
TTAATTACAACTATGGAGCAGTGTTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT
GAACATAATGAAAAGGAGTACTGCTTAAATCTTCATCAGCTTTCAAAATATCATAGAA
GGAAGTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTTGAGGTATAC
AGAGTGGAGATTCAAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT
ATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGGCCTGGATTTCATGTCTC
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGCTGAAGATCCTCCACATCACTA
AAGTCCTTCAGGTGTCCTTCTCCTCTATTCTGGAGAATGTACCAAGTATTCCAGTGGA
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
ATGACTCAGAAAACCTCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTTCTTCTTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
ATAGATCCTTCTTCAGAAGCTCCAGGGCATCTTGCAGGAGCAGGCCAGTGAGAGCAGC
TGTTCTCCAAATTTTCTGGGATGAATATGAACAGTACAAAAAGAATAA

SEQ ID NO: 77_AA840598_M IRAKM_M

ATGTGGAAGAGATTTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG
AGCAACGGGACGCTTTTCGACAGATTACAGTGACAAATGGCACAACCCCGCTTTCCTGG
CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGCACAACACT
CAGCCGTGCGCCGTCATCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG
CTCCAACCCAACTAACGGATTTTGCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACACGTTTCAGCTGCGG
GACCTCCTCATGGAAGTATGAGAGAAAAGAGGCCTAGACTCCTGCCTGTCTTCTTAGAC
AGGAAGATAACCACCTGTCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG
AGCACCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCACGTCCTTGAAGTCCTTCAGG
TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGAAGTTCAGAAA
ACCCCTTTGAATGCAGCCAGTCTGAGGTACCTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
CTCTTTTGCAGTGAGCATGAACAGTCCAAAAGCAGTGAATCCACCAGAAGATCAAGCAA
AAAATAAAAGCAAACGTCACTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCCTTCCCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTTCTGACAACCAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA
CCCACCTTCCAGAACCAGAACCACCTTCTCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCCTTTTATAAAACCCAGGTCTTCAGGGCCCCACCCCTTTCTTTTCCATCCTTGCT
CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTGAGATCATTTGCACAAGAACA
AGCGAATACACAACAACAAGCCCACCATCATTACCACCGGCACCTTAATGCTAGTCTTTC
TGCTAGGGATACTGACAGTCTATTTGCTTCCCATGGTCATAGGGAAGTTGCTCAAATGCA
AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT
TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCAGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAAA
TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78_AA088547_H

ATGGCGAGTGCGGTCAGGGGGTTCGAGGCCGTGGCCCCGGCTGGGGCTCCAGCTCCAGTTC
GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTTCATACTCTCAGGCCAGAGAACCTC
CTGCTGGTGTCCACCTTGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG
AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC
TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA
TTAATGAAACTGCCATTACCATCCCTGAGCTGGTTTCATGCCTCTCCCTGCCGCAGCTCT
GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGTG
TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG
CGCCAGCTGCCGCATCTCACGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG
GGCCACATCCGACTGCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG
GACACCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCCACCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCCAGGATGCCCAGTCCCTGCACTCG
GGGGCCAGCCGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCGCGGGGCAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGGAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCCTCCTTGCAAGGAGTACGTAGAAAAC
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTGCTGCTGCAGCAGCTGATGTCTGGC
CTGGCCCCACCTGCACTCTTTACACATAGTGCACCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGCTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCCTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTCTGCTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCGCAGCCACGCCCCCTTGCCCCCAGGTGCTGGCCCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTTATAAGGGGACA
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC
CGCTTCCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
GGGAGGTGA

SEQ ID NO: 79_HGP_6644466

GGAGGGTTCGAATTGCAACGGCAGCTGCCGGGCGTATGTGTTGGTGCTAGAGGCAGCTGC
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT
TTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAAT
GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAAACATTGTTGGTTATCG
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC
CATAATTTTAAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAAGGCGATTTTGAAC
AATTAAAATCTGTGATGTAGGAGTCTCTTACCCTGGATGAAAATATGACTGTGACTGA
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCAAAGAAGCTGTGGAGGAGAA
TGGTGTATTACTGACAAGGCAGACATATTTGCCCTTGGCCTTACTTTGTGGGAAATGAT
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAACTTT
TGATGAAAGTGATTTTGTATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATAACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

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FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAACTTAAAT
TGAATGACCATTACTTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA
TTAATTTGTACCTTAAGCATTTCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

SEQ ID NO: 80_AA449542_M

ATCTCCAAGAGGGTTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAAA
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAAGGTGATTTTGAAACAATTAAAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
ATGGAAACCCAAGGAAGCGTTGGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCAATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAACTTGTATGGGAAGTGTAACTAGATATATGTAGTTAATATACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACTAGTAGTACCCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTTAGATATTCTTGCTTCTTTAGTGGGTTACTAAAAAT
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTTCAGCTGGC
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTCATAAACGTAGCTCCTAGGGTGTCT
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTTAGTACCAGG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT
AGCAGTGGGCCTCAGCTACCTTCACTTCAAAGGCATTTTCCATCGGGACCTCACATCAA
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82_AA232253_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTGAA
AACTGCGGTGGAGGAAGTTTTTGGGAGTGTATTCGAGCCAAATGGATATCACAGGACAAG
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTC
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATT
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTT

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FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCATAACCAT
ACAACACACATGTCCTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT
CTCCCTGTGTCAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA
ACAAGGGAGGTCCCCTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGA
AAAAACGAGAGATTAACCATTCCAAGCAGTTGCCCCAGAAGTTTGTCTGAACGTGTACAT
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTG
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAACCTCATTCTACACAACAAG
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
AAGCTGACAGAGCAGTCCAACACCCCCGCTGCTGCCTTCTTTGAGATTGGTGCATGGACG
GAAGACGATGTGTATTGGTGGGTTTACGACGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACTTC
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAACCTG
GTTTTTGGTTTTCACTTGAAACCAGGAACTGGCCACAGGATTGTAAGTGGAATAATGTAT
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACT
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTTGTAATGGAGAAGTGG
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCCTGTACATATGAGAGTGATGTT
AGAACTCCAAAAAGCACTAAACATGTCCATTTGATTCACTGGAGTAGAACAACCTCAG
GATGAAGTGAAAGCAGTCCAACCTTGCCATTCAGACATTATTCACCAATTCAGATGGCAAC
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG
CAGATTGCATCCAACACTTCTTTACAGCGTTCCCAGAGCAATCCTATTCTGGGGTCACCG
TTCTTCTCACACTTTGATGGCCAGGATTCTTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCCTACTCAG
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTCGATACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCCTAGAGGAAGATACAGTGGAAGAGT
CAGCATTCCACTCCATCAAGAGGAAGATACCCTGGAAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACCAGGGATGCCTTTGCACCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGAATACCGGAAAAAGCCCCACAGGCCA
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT
TGA

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ATGGGAAATTATAAATCTAGACCAACCCAACTTGTACTGATGAATGGAAGAAAAAGTC
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAA
GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAACCTCGCCTTCTTTTGAATTTGGTGCTGATGTAAATGTAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAGGATTCTTGAATATTGCAAACCTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCCTCCAT
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTTGGAA
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAAACATCTTCAGTGAAACAGCTTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTTCGCCTGGTTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTCACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGGGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCCATCTTCAGCTC
TCAGAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCCATTTCGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAGAAGTCGTTTCGAATTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT
TTGTCCCAAAGTGCTGGACAATATTCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

ATGATTTCTTGCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTCTCTGTATTCTTTTTCAAAGTGCC
GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAACGTGTTGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCCTGCACTGCCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACCTTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTCGGAACCCCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACAGTAATTATCTCAAACAGATCTTAAA
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTCAGTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCATATGGGTGAGCCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCAGGAAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTTGCAGCCAATTCCGGACTCGGCTCAATAGTTCCACAGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTCCGAAAGATCATGCTCCCCGCCTGGCCCGCCTTCTCTGGAAAGCCGTTT

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FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTCAGTCATTGACTACAACTA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCCTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGGAATTCCTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCCAGAACGCTTTCCTGTGTTTGATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTGCGCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAACCTGGTGCTTGCTGGGAACTTGGAACCTTCCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTCAGCAGCTCACTGAAGCGCCAAGCTAT
CCCTTTAGCAAAAAAGTGTCTCAGATGTGTAAAGCTGAGGAATGTGGTGTCTGGCTTC
ACAAATGAAAAGGAGGCAGATGTT

SEQ ID NO: 85_W20810_M

TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA
CAGTGTGTGACAGGCAGAGTCGTCCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA
CTCCCGGCTTGGA AAAACTGAAGGAGTTAATGATTCAATTGCTGGGGTTCCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACC AAAAACCAATGAAGTTTACAATCTGGTAAAGG
ACAAGGTAGATGCTGCTGTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG
GCAGAAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCCAGGG
AAACCATGGTTTCTAAAATGCTGGACCGCCTGCATTTGGAGGAACCTCCGGACCAGTTC
CTGGAAAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCCTCACCCCAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCCAACGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCCTTGG
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA
AGTGTGCCATTCAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCTGAAGCTCACAACTTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTG

SEQ ID NO: 86_AA744236_H

ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACACTGAGAGAACCACCATTTACCTTA
CCCTCTGGACTTGCTGTTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT
GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTTGAAGACACTT
CGTCACCCTTGCTTGCTAAGATTTTTATCTTGTAAGTGTGGAAGCGGATGGCATTCTCTT
GTCAGTACGAGTACAGCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGGAACTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

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FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACCT
CTCCCAGAGTGTCTATGGACATGCCCGGGATGCCTTTTTCATTTGGAACATTGGTGGAAAGT
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA
TTGAAGAGTGAAGAGGAGAAAACGGAATTCTTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTTAAGAGTTTCTTCCCTTATCTGCTTGGCCCCAAAAAAGATCAT
GCGCAGGGAGAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTCTGTCTCAC
ATCGAGGCCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
TTCAAACGCACTGCCCAAGTTTTACTAAAAATACTGACCTTTCTCTAGAAGGCGATCCA
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAAATACTTCGGAG
GACAGTGAAAACCTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAACCTGTCAACATACAGATTTGGCCTAGAGAACCTTGTGAT
GATGTCAAGTCCCAGTGCCTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTCAACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAGTAAAAAAGAAGCCAGTAAAAGATCCTGAGATGGAT
TGGTTTGCTGATATGATCCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCAAAAAGGATGATGTCTCCCAGTGATGCAGTTTTCCTCA
AAATTTGCTGCAGCAGAAATTAAGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAAGTGGGAAGATAATAACTGGTGA

SEQ ID NO: 87_AI052250_H

AGCGGCCGCGGGGGCGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA
GGCAGAGCAGGAACAGCCAGGAGGCGTTTATTAGGGGGCGGGGGGAAAGAGCCCCAGCA
CCGCCCCCTCCTGGAAGAAGGAAGAGGTAACATACTACCCAATATTGCAGCCATGGAGT
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCAG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTCGACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGGAAGATTTTAAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTTTTGATAAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
CTGTCCAGCATCCTTTAGAAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAGTTT
TTGCCAGTTTtagccaatgTTCCTTGGTAACTGGGAAAATCTACCTTCCCCTATATCTCCAG
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG
AAGGATTGTCATTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA
ATATAATTTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCCAAATTTAC
CTTCATTGTGCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTCGTGAAC
ATGTAAAGCTACTGTTAAATGTAACCTCCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCAGAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAAC

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FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGCAGAGAATTTTGCCTTGTTTGACTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGTGTTTGCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCTGAACTTGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTAAATTTTCTACAAAAAATGGATTTGCTACTAACCAAAACCCCTCCTG
ATGAGATAAAGAACAGTGTTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG
GACCCGGAGCTAAGGCGCCCGAACCCGCGGCGGCGGTGGGGACGATGTGGTTCTTTGCCC
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGAGCCCCCAGAGGGCGGCCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
AAAAATGCCTCCACGTCTGTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA
AAGCCCTCAGCTTCCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCCG
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGCCCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCATTAAGTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGTCAGAACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGAGGAGATTTCAGATCAAAG
AGCCAGCCGAGAAGCAAAAATTCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTGCGCACAAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTTGTCTCACGCCCCCTCTCAAGGTGGGCAAGTTCCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCTCCTGACAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTCGTACATGGCTTCTGACACCAACCTGCCATCCGGG
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCTTACCTCTGCCTTACGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
CGGGTGTCTTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTCGGAGCTTCTGTCCAAATTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTTCGACCCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG
GAGTTCCTGCCCCAGCCCCACCCCTGTTCTGCAACCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTCAGCAACTCCGACCACAAATCCT
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGTGCGGAGAGCCCGCCCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCGGCCGCCAGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTTCAC

SEQ ID NO: 89_AA599286_H

ATGGCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG
CAAGGAGGAATTTCTGTGGAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCCAAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT
CCAAACAACATATTCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACCTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG
GCTGACCTTGGCCCAGACAAGTATTTGTCTAGATAAAGATTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTTTGACCCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG
GAACTCCAGCAAATAAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCGGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCCTTCTACCGATCTTAT
TTTTCACAATTACAGGAAAATCAATACATTGAAAGTGTGGATGTCCACTGCTTTGGCCAC
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCTT
CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
AAAAATGGCATGCCTACCATCTCCCGGCTCTTACAGATGCCATTATTCAGCGATGTTTTTA
CTAACCCTTCTGAAAAACCAACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTCACCAGCAT
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
ATTTTAGCTCGAAAGAAGTCAAACGATCTGCTCTTGAAAATAGTGAAGAGCATTACAGCG
AAGTACAGCAACTCCAATAATTCAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG
TCATCGCCAACCTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCACAGCAGCTCCCTTGCCCTCTGCGAGCACCGAGGCACCTGCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCTTGCTCAGCTCCATCCAGAATTTCCAA
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGAGGGGAAAAGTTCTTTTTTATTCTACTACCCCTACCCCCAAC
TACCCTCTTCTTGGAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
TCACAGGCCCTCTGCGGGCCCGAGTCCTCGGGCTCCGAACTAGCCCTGGCCACACCGGTG
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC
TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCGCAAACCTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTGACCCCAAAAGA
GAGACCATTTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

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FIGURE 2TTT

TGCATGGTGTCTGGAGGTGCTGGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACACTAC
CAGGGCCTGCCCCTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGACGCGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCGGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGCACTTCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG
GCCACACAGTTCAGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCACCCGCCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGA
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAACACCAAAGAAAAGTGGCAATTAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCCGACGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGGCAAGGCCCTCTTCCGTCAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTGTCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAG
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAGCAAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC
ATCAAAGAAAAGTGGCAATTAAAATTATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGATGGAAGTGGCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGGCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCCC

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FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATAACCCCATGATAGCAAGAAAGGTG
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAAGTCTG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTGGAACATGGGACCTTG
AGGAGTTCCGTAACCAAAAAGGAGAAAGTAACAACAGCCAGTGGAGACAAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTTCTGGAAGTGGCTCAGGGTGGTGTATGTCCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGCACCGGGACTTAAAGTTGGAGAACCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGGCTTTTCCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACACTCTAGTGGTTCGCCCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATAACCATCTCCCAGGAGTGCAAGGTCCAAGTCTCATTGCCTGTGTGG
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCTTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTGACAGCCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG
GGGGATGTAGACGGCAGCGGCCAGTCGCTCCTGGCACCATTGGACGATGCCACAGTCCT
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCTCCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCAGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGCC
CGACCACCGGCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTGCGGGTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC
AAGGTGGTGGACCGGCGGCGAGCGCCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAAGCGCGCGACCTCTTTGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCACCC
GAGGTGCTCCTGGGCATCCCCTACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTATGGTCAACGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCGGGAGCTCCAAAT
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTCAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTTCCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC
CGGGCGCAGCGGGGCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGACAGTTTGAGGAGTGCCTCCTGCAGCGCAATGGGTTAGCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTCTGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT
AGAAAACCCAAAGATGGAGTTGCACATCCCCCAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT
TGAAGTTGAAACCAGAATGGACCAGGTCACATGTGCTGCTTAAATTCAGGGCTAAGCAT
TTTGGGTGATTTTAACTAGGTCGATTCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGGGTTTCCCGCTTCTTTTATGTTTTGCTTTATTTN
TNNCTTTTCTTTTCTTTTNTTTNCCACNTNCCTTTTTTTAAATTTAAACCATTTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCGC
AGAGGGACAAAAAGCCCGGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG
AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCTGGCCCGCGCGCGGCCGATGGCGGCGCGGGGATGTTCTGACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGAGGAGTGCGTCTTACAGCGCAACGGGTAGCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTACTGTGAAGGTGGAGAC
CTCAATCAGTATGTCCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA
CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAACCATCGTGACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTC

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FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAACTCCAGGGCTGAACGTCTTG
GGTGTTTTAACTAGGTTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
CACGCTTGGGCTGCCACTCTACCCTTCTCTTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAAGCCGGAGGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC
GCGCACCACGGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGAGGCGCGAGC
TGCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT
TTGTGGTGTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGGTTGGATACCAGTGACTTGGAAACCTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTCAGTGTAACAAGTGTTTC
CTTTCACAGCATGTGGAACAGATTTTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAGGATC
ACATTCATAGACACAGAGACAAAGAAGGAACCTTGGGGAGTTATGTAAACAAGGAACCT
GAGATTGTGCCTGTTGGGGAGGCACCTTCTGGAAAATCCCAAATGGAACTTCTCATTCCT
GTGAAGAAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA
AACCCTCAGGATCGTCCAGATGCTTTTGAACCTAGAACTCAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAAATACCATGGATGATATGCTG
CTTCTGTTTAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC
TACCCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTTCTCCTCATTTTTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAAATGATTATTGATAGAAGTTTGGCAGGAAAATTCTTTAAGAGCTAACAAGAGAAGA
GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG
AATTTCCATGGGAAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCTACTCTGCCCCCTCCC
CCTAATGAAATCATATTAAGTNGTTTTCTCTNNTTTTTTTGTAATATACAGCTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAACCTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
AGGCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC
TGCAATTTCCGGCGGGCGGCGCTGGGGGACAGCGTGAGCCACCCAGTGCTCGGCCCCGCCCC
GCAACCCGCCGGAACCGCCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCGG
AATGGCGGGGCCCCGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTACCGAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

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FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATAACCGCAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT
CGCACAAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGCGTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT
AGCAGCCGCCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA
TGAAGTGGATGCCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCCGAGACCTGCTCAGAGAGATGGCCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCCGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
AGGCGGGAGCTGCTTCACACTGAGGTTCAAGACCTCATGGCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGGACTGTGCGAA
TCTGTTTCGTAGCTCTTGACCCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACTAACCCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGATGGACAGTGCTGAGACCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGTATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGT
TACTGGGTCTGTGCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCTGGCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCCTCCCCACAGTATGCACTCAGCC
CCACAGAACCCACCAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCTTGGTCTCATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
GGGAGAGGGAGGCTTGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCGTGAGCCCTGGGCAAGCTCTTTCCCCTTTCTGGGCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTCACAGCCACAGCATGGGCACTTATGAGGACAAA
GTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCCTTGGGCAAGAGCTGTCTGTCTCC
TGCAGGAGGCTGAGTGTGAAGAGTATCATTATTGTTTCTCTATTAAATTATTTTCTCT

SEQ ID NO: 101_AA311714_H

TGGACCTGTCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA
GAAGTCGGCCCAGAGATGGAAAACCTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTACCCGTGAAATAAAACAC
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGAATTACAT
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGGA

FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTTCAGAATTAAGTGAAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCAATTTTGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAAGTGAAGTTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCCTACTCCCAGAACTAGC
ACTGCAGTGGAAAGTAAGTCCTGGTGAGGATATGACTCACTGTTCAACACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
GAGCTTATCTACACGGACTCAGATCTTGTTGTACCCCCATTATCGACAATCCAAAGATA
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGC
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG
TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACACAAGTGAAGTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACACTCCACT
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA
AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGGGGCTGGTCAGCGGCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103_AA210451_M SGK384_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTCGGCTGTAGA
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC
TCACCGAATATCACCCCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA
TCATTAAGTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAAACATTGTCCAGTACCTGCTAACAAGTAAGTTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTCGCAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTACGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTCTGCTCTCCTGGCAGCCCCG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACAAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTTCAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTTCCTTCTCGCC
CACGACCCTTACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATCCAATCATCACACACTCAGAG
AAACTGTCTGCTGCTGGCAAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCCACACCTGAGATTAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACTTTCTTACCTGCCT
TGAATGGTGCTTTGAACTTCCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
GAACCAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC
CAATAAAAAAACAAAAAGGTC

SEQ ID NO: 104_SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAATGCATGGATGACCATTACGCCAGTCAGGCC
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCACATCTCTGTGTACCAGGAG
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGATGGAGTTC
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTGGATGGCCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC
AGCCTGAAGGCCGCTCCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCCCTCGTGCGTCTCTCTGACCCTG
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAAACTAGGGAAGCTGTTGGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGTCTTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTCATGGTCTACAGCCTGCTAGCCATCACCAACCCAG

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FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAAGCCCGGGAACCCAAAGAACCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTGACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCCAACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACTTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGAATAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTCTGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA
GCGGAGCCGCTCGGAGCCTGAGCCGCCCGGGGCGGGGCGGGGAGCCGCGCGGGGGCCG
GCCGGCCGGGGGAGGGGAGCGATGCGGCGCCGGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTCGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGCCCCGGCCCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCCGGGCCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCACG
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCTTGGGAGGATCGATTC
CGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCGCGCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGCAGGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCTCCCTGGGACGGTTCGGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCCAGGCCAGCCCAGGGGTGAGGGGCAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTCTGCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTAT
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC
T

SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG
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CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG
GCTGCTATCGCCTGGCGGCCCAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCTTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCGTGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCTGTG
CAGGCGTGACTTGTCATCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTCAGTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCCTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTTCATTAAATTGTTTATTTTTGTAAAAAAAATTAAT
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA
CATGTGTATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGTTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTCAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGCAGCGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTCAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGTGAGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTTACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTCATGTAATGTGAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGAGCAGCCAC
TCCACTCCCTATGGCATTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAAGTGTTCATCATTTGACAATAAGCGCTAC
CTCTTCATCCAGAACTGGGGGAGGGTGGGTTCAGCTATGTGGACCTAGTGGAAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCA
GCCAAGGGTTATGCCACAGAGACTTGAAGCCACCAATATATTGCTTGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCATGAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCAA
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC
GACGGCTGCGGGGGCACC GGCGCGGCCACCATGGCGGTGCGACAGGCGCTGGGCCG
CGGCCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTACGGGCAAGCCCGGCGGGCCTA
CGGCTTGGGGCGGCGGGCCCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGCTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTTCGTGGTGGCGGC
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTTCTGGCCTTCGGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA
GGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCACTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGGCCAGGTACCAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCAGCCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCCTGGTTCGACTACCCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT
TGTCATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGCAGCTACCAAGAGGC
TCAGCTACCTGCACTGCCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAACAACAAAATGAAGATGCTCTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAAAGGCCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTTCACTCTGCAGTCCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCTAACACGAGGAACCTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTTCAGCACGTTTCACTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAATGCAAATTTACA
ACTGCAGATGACGTATGTGCCTTGAAGTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTTATGTC
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SEQ ID NO: 112_AI086865_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
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CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAAATGAGTGCCAGGTCCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTTATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCGTGCAGATCCTGCTTGCACTGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTTCGTCAAGATCGGTGATTTTCGGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC
ATCTGGGCCCTGGGCTGTGTCCTTACGAGCTGGCCAGCCTCAAGAGGGCTTTCGAGGCT
GCCAATTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCAACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGCTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTTCGCCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXAAAGAAGAGGAAGAGGAGGAGGAGGAGGAAAAGCAAG
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATT
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGCGAGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG
AGGGAAGGAAGGGGCACAGCCCTATTTCTTCCTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
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CCC

SEQ ID NO: 113_AA836348_H

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GGCGGCGGCGCGGCGGAGCAGGAGGAAGTGCCTACATCCCCATCCGCGTCTGGGCCGC
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTTCA
GATTGTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAATGGTTCATTTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACCTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATTGCTGTAGTAACATCACGAACCACTGAAGTCTATGTTTGGGGTGGTGGAAAATCC
ACCCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTTCACAGTGGAGAAGGAACTGTACACTTGGGTGAACATGCAA
GGAGGCACTAAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTGATGTGGTGTGATTTTC

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACCTACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTTCAGAACTCTGAGAAAGATAACCTGCCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTGGCC
TTTGAATCACAACTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H

ATGAACTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
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TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCAGCCTTCACTCAGGCATCAAT
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGAGAGAAGATGCAGTAT
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCACGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTTGCCAACCATTCAGACA
GCCTGTGCCAGGGCGACCAAGTGCTTGGTGCTGGTCTTGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCTGGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCAGTCGCCTCCATATGCGGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGATTCCACGGCGCCCGCGGAGGAGGCGGAGGGCGGGGGAG
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGCTGGGCAAGGGC
ACGTATGGGGTGGTGTACGCGGGCCGCGATCGCCACACGAGGGTGCGCATCGCCATCAAG
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCTGCATGAAGAGATCGCTCTTCAC
AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGGCTAC
CTTAAGATCTTCATGGAGGAAGTGCTTGGAGGCAGCCTGTCTCCTTGCTGCGGTGCGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGCACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAAGTCTGCAGTATATGGCCCCAGAA

FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCATTGAGATGGCCACAGGTCGCCCCCCTTCCACGAGCTCGGGAGCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCCAGCTCTCTGTGGCC
GAGGCCCAAGCCTTTCTCCTCCGAACTTTGTAGCCAGACCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCTGTCAGCCTGGGAAAAGGAGCCGAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCTCTCAGCACCCACCCAGC
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTGCGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCTGTTCTGGAATCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCAGGTCAGAGGAGCTGAGTAAT
GAAGGGGACTCCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCCTGGCCCCAGAGCCTCCAATGCTCTTTCAACG
GACCAGGGCCTGGTGCAGTGGCTACAGGAAGTGAATGTGGATTGAGGCACCATCCAAATG
CTGTTGAACCATAGCTTCAACCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA
AGGAAAGAAAGCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG
AGAGCCTCGAGTAGCTCCCTCTGGATTATTCAATTCCAATTCACACCTTCTAGAAGTGA
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC
ACCATGCGGCAGAGGTCCAGGTCAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
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CAAAGCAAATCGGGCTATTCTCAAGCAGTACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTAACCATCACCCCTCCCTGCAGAGCAGTTCGCAGTACATCTCCACGGCTTCTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCAGGGGAATACTTGGCCAACTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTCGGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTACAGGGACATAAAAAGTGACTCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCTACTTCAATGAGCCTCCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTTAGACTTGATG
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGACATCCATTCTTA
AAACTAGCAGGTCCACCGTCTTGATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

SEQ ID NO: 116_SURTK106_H

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AAACTAGGAAGGCAAGGAATGGCAAGGTCAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTGTTGGTTACTATCTTCCCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCCTGTT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
AAGGAGACATCCGTGGAAACTTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGGCC
ATCTTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG
GCTTTAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG
CTGCCACTCTATATGGTGTGGAGGATGTGGCCCAGGGGGACCTGCTCGGCTTTCTCTGG
ACCTGTGCGGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTTG
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC
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ATACCTCTCAAGTGGCTTGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT
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CCCAGTAGCTGCACACATAACCATGTACAGTATCATGAAGTCTGCTGGCGCTGGCGTGAG
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GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACTATAGCATGCTTTGAAGAGTCTCGGGC
AAGAAACATTCATGCATGAGTATATGTTCTTGGAATCAATTCTCTAAGAACAGAGAATG
GTCTTTCCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCTTTACACA
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA
CTGTCACTCTCACTTCTGCTGTCCAGTCCTAGAAATCCTGGGTAGAAGTGGTGGACCTG
TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACCACATTTTATCTAGATGAAAATTTGGAA
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA
AGTTCTTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTTCATGATTAA

FIGURE 2KKKK

GAACATTCAACATGTATTGTTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT
TTCAATCATCTGTTGATATACTGTGAAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117_AA098024_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT
GACCTGACTCCCAAACCTTTGTTCATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCCTTGGGATCCTGCTTTATGAGATG
GTGACTCTAGGAGCACCACCATAACCCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTTCAGCTGCTCCAGCGC
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG
GTGCCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTTCTATAGCTTC
AGTGTCCTTTGAAGATGGTCTTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA
AGAACAGAGAGAAGGAACCTTTCTGTGGCCACCAAGGGAGAAAAAAGGACATGGATCTTG
CATCTTTCCCTAAACATTTTCTTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGGCTTTCCAGTCCCA
AGGGCTGAAGTATAAGTGGTGGACCGTGTCATTCTAAAGGAGGTTTTTAAATCTGCAAT
GATTGTAAGGGAATTAGGCAAAAGGGCTGGTCCCCTCACTCCAGGCTGGTTTACTACTG
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ATGGGCATGAATGAACACCTTCTAATTTTTTAACCATGAATTGAATATTGGAATTCATGAG
AAAGAAAATTCTAGGTTCTTTTTTGCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA
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GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCTTTGACTATAGATAGAAGAGCA
TCCTTTTCAATTGAACCTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAAATTAGAAGCA
GGAGGAGTCATTTTCATGATTAGGAACATTGTTTCATCCCATTTGTTTGCCAGTTCCTGTAA
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TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAAGAGGCTAAAAGAAAATAAATGGGA
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAGAGATTCTTTATGTGCA
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SEQ ID NO: 118_SGK2ALPHA_H

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CCCACGGACTTCGACTTCTCAAAGTCATCGGCAAAGGGAACCTACGGGAAGGTCTACTG
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAAGTCCATC
TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
CGGCACCCCTTCTCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGTTTC
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC
TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGACTGCCAGGGA
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGTCCTCTACGAGATGCTCCATGGCCTG
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG
ACCTGTGAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA
GAGCGACTCAAAC TAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA
AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTTTGATTTTGATCT
CAATGTGTAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTT
TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H

ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGGCGCCACGGCATCGTCTTCAAG
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTTG
GAAGACGGCTTCCCTAACCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC
TTTGAGTTCATGCTGTGCGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGCC
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCTTCTGCCATGCC
AACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCCTCAGGCCAG
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCCAGACGGCAGCCGCCTCTAC
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC
CCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC
ACCCCAAACCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC
TTTAAGGAGCAGGTGCCCATGCCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCAGGCA
TTGGATCTGCTGGGTCAATTCTTCTTACCTCCTCACCAGCGCATCGCAGCTTCCAAG
GCTCTCCTCCATCAGTACTTCTTACAGCTCCCCTGCCTGCCCATCCATCTGAGCTGCCG
ATTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT
GACTTCCACGTGGACCGGCCTCTTGAGGGAGTCGCTGTTGAACCCAGAGCTGATTCGGCC
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TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTCACCCTCCAAGGCCTCCCCATGGCC
ACAGTGGGCCCACACCACACCTTGCCCTTAGCCCTTGCGAGGGTTGGTCTCGAGGCAGA
GGTCATGTTCCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTTCATGGCCT
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT
GCTGCCAGTCAAGGCCTGCATATGCAGAAATGACGATGCCTGCCTTGGTGCTGCTTCCCC
GAGTGCTGCCTCCTGGTCAAGGAGAAGTGACAGAGAGTAA

SEQ ID NO: 121_TESK2_H

GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA
GTCTCCTCGTTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
TCCCTCTTTGCCGCCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC
CTGCCTCAGTGTCAAACCAGAAGAGAAGTAAAATTCAACAAAAATTTATGTGTGGAGTTC
CTTCTTAAAGAAGAAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTCAA
TTGCAGGATTTCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAAATAGGGTCTGGCTTCT
TTTCTGAAGTGTTCAAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA
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GCTACCTTCACTTCAAAGGCATTTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC
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GGAAGCTGCAGCCACAGCCAGGGGACTCTTGGAGAAAGCACCTGGGGTGAAGCGACTAA
GCTCACTGGATGACAAGATCCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCCACGTACAGTGAGTGTCTTGGACC
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GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCCACCATTCCGGGCATCTGCCCTAC
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAAATGGTTTTG
GGTCCAGGCCCCAGGGGACCAGTCCATGCCCTGCGGGTGCTTCTGAGGAGATGGAGGTAG
AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAAA
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTTAGTCCCTGCCTCACCTTGGGGATGGACCT
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTCCAGTGCCCATTTGGCTGTG
TATGACGGGAGGCAGCAGTGAGAGGCCTTCCTAGTTAGGGCCAACAGCTGATACCAAGCC
TCTGAAATCCAGCAAGGAGGTCTGCCTCCCACCAGACCCTCTCCAGTGTAATCCCCAGA
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT
TCCCCACCCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA
TGGAGCTGATCAAGAGGCCGTAATGGTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCACCTTACTGCATGGTCAGAC
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTCATGGCTCTTAG
CTAACCTATTCAAAGACCTTTTCTGTGTTGATTAATCTATTTTCATATTTATAAAGGAGTC
TTAATGTTCTGCCCCATAAGACTTTCAACCTTGTGGTGGGAGTGGGGCTGGTTTTGTAG
GCCCTAGGGCCTGCTTCTATGTATTTATCAACATGTGATACATTCAATTGGTTAAATGGT
TTATACAGGGACTGATTTGCTTCCCTTCTGCCATGGCTGGAGCTTTGGGAACAGTCTGT
CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTCATAACT
TGCTTCTGTTGATTTTTTTTTTTTGTAAAACCTTCCCAAGACATTTTCAGACTTAAAAATAA
AGTCAGTGTTACAGGT

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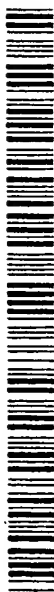
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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to kinase polypeptides, nucleotide sequences encoding the kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.



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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER

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 A61K38/00 G01N33/68

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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, EMBL, MEDLINE, BIOSIS

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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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International Application No

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E	WO 00 55332 A (INCYTE PHARMA INC ;AZIMZAI YALDA (US); YUE HENRY (US); AU YOUNG JA) 21 September 2000 (2000-09-21) SEQ.IDs. 7 and 21 DOC. AGAINST INV. 6 (SEQ.IDs. 127, 9) SEQ.IDs. 2 and 16 DOC. AGAINST INV. 26 (SEQ.IDs. 147, 29) ---	1-15, 26-30, 35-38
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Int. l. Application No

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Int .tional Application No

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P, X	WO 99 33961 A (AKIRA SHIZUO ;KAWAI TARO (JP); ASAHI CHEMICAL IND (JP)) 8 July 1999 (1999-07-08) SEQ.IDs. 5 and 6 DOC. AGAINST INV. 26 (SEQ.IDs. 147, 29) SEQ.IDs. 29 and 30 DOC. AGAINST INV. 40 (SEQ.IDs. 161, 43) ---	1-14,16, 26,27, 29,30, 35,37
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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X	WO 98 01756 A (UNIV WASHINGTON) 15 January 1998 (1998-01-15) SEQ.IDs. 1 and 2 DOC. AGAINST INV. 30 (SEQ.IDs. 151, 33) ---	1-14, 16, 26, 27, 35, 36
X	DATABASE EMBL 'Online! Accession Number W90839, 9 July 1996 (1996-07-09) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:420441 5' similar to gb:M80359 putative serine/threonine protein kinase." XP002165856 abstract DOC. AGAINST INV. 31 (SEQ.IDs. 152, 34) ---	1, 2, 4, 6, 7, 10-13, 16
X	NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES. IV. THE CODING SEQUENCES OF 40 NEW GENES (KIAA0121-KIAA0160) DEDUCED BY ANALYSIS OF CDNA CLONES FROM HUMAN CELL LINE KG-1" DNA RESEARCH, vol. 2, no. 4, 31 August 1995 (1995-08-31), pages 167-174, XP000676653 ISSN: 1340-2838 the whole document -& DATABASE EMBL 'Online! Accession Number D50925, 1 August 1996 (1996-08-01) NAGASE T. ET AL.: "Human mRNA for KIAA0135 gene." XP002166244 abstract DOC. AGAINST INV. 32 (SEQ.IDs. 153, 35) DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36) ---	1, 2, 4-7, 10-14, 16
X	DATABASE EMBL 'Online! Accession Number U79240, 14 December 1996 (1996-12-14) YU W. ET AL.: "Human serine/threonine kinase mRNA." XP002165857 abstract DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36) ---	1, 2, 4-7, 10-14
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X	<p>DATABASE EMBL 'Online! Accession Number AI036899, 29 June 1998 (1998-06-29) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:1746011 5' similar to TR:Q99763 serine/threonine protein kinase." XP002165858 abstract DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36)</p>	1,2,4,6, 7,10-13
X	<p>DATABASE EMBL 'Online! Accession Number AI469033, 17 March 1999 (1999-03-17) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2137322." XP002165859 abstract DOC. AGAINST INV. 35 (SEQ.IDs. 156, 38)</p>	6,7
X	<p>DATABASE EMBL 'Online! Accession Number AC007225, 7 April 1999 (1999-04-07) BRUCE D. ET AL.: "Homo sapiens chromosome 16 clone RPCI-11_480G7." XP002166245 abstract DOC. AGAINST INV. 37 (SEQ.IDs. 158, 40)</p>	6,7
P,X	<p>WO 99 49062 A (FAN WUFANG ; GENE LOGIC INC (US); PRASHAR YATINDRA (US)) 30 September 1999 (1999-09-30) SEQ.IDs. 1 and 2 DOC. AGAINST INV. 37 (SEQ.IDs. 158, 40) DOC. AGAINST INV. 55 (SEQ.IDs. 176, 58)</p>	1-14, 26-30, 35-38
X	<p>DATABASE EMBL 'Online! Accession Number AI596766, 26 April 1999 (1999-04-26) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:949322 5' similar to WP:ZC373.4 CE02377 myosin-light-chain kinase domain." XP002166246 abstract DOC. AGAINST INV. 38 (SEQ.IDs. 159, 41) DOC. AGAINST INV. 39 (SEQ.IDs. 160, 42)</p>	1,2,4,6, 7,10-13, 16
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X	<p>KAWAI T. ET AL.: "Duet is a novel serine/threonine kinase with Dbl-Homology (DH) and Pleckstrin-Homology (PH) domains"</p> <p>GENE, vol. 227, no. 2, 18 February 1999 (1999-02-18), pages 249-255, XP004158739 ISSN: 0378-1119 the whole document DOC. AGAINST INV. 40 (SEQ.IDs. 161, 43)</p>	1-14,29, 30,35-38

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X	<p>DATABASE EMBL 'Online! Accession Number AA454060, 11 June 1997 (1997-06-11) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:795492 5' similar to TR:G49075 calmodulin-binding protein." XP002166248 abstract DOC. AGAINST INV. 41 (SEQ.IDs. 162, 44)</p>	6,7
X	<p>DATABASE EMBL 'Online! Accession Number AI385971, 29 January 1999 (1999-01-29) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:514336 5' similar to WP:R90.1 CE06325 protein kinase." XP002166249 abstract DOC. AGAINST INV. 43 (SEQ.IDs. 164, 46)</p>	1,2,4,6, 7,10-13, 16
X	<p>DATABASE EMBL 'Online! Accession Number AA436054, 1 June 1997 (1997-06-01) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:730582 5' similar to gb:X66363 serine/threonine-protein kinase pctaie-1" XP002166250 abstract DOC. AGAINST INV. 44 (SEQ.IDs. 165, 47)</p>	1,2,4-7, 10-14,16
X	<p>DATABASE EMBL 'Online! Accession Number AA061797, 24 September 1996 (1996-09-24) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:513953 5' similar to gb:X66358 serine/threonine-protein kinase." XP002166251 abstract DOC. AGAINST INV. 45 (SEQ.IDs. 166, 48) DOC. AGAINST INV. 46 (SEQ.IDs. 167, 49)</p>	1,2,4,6, 7,10-13, 17
A	<p>WO 98 35015 A (GERHOLD DAVID L ;MERCK & CO INC (US)) 13 August 1998 (1998-08-13) SEQ.IDs.2 and 3 DOC. AGAINST INV. 50 (SEQ.IDs. 171, 53) DOC. AGAINST INV. 114 (SEQ.IDs. 235, 117)</p>	1-30, 35-38
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P, X	WO 99 38981 A (AKERBLOM INGRID E ; INCYTE PHARMA INC (US); CORLEY NEIL C (US); BAN) 5 August 1999 (1999-08-05) SEQ.IDs. 3 and 9 DOC. AGAINST INV. 51 (SEQ.IDs. 172, 54) SEQ.IDs. 6 and 12 DOC. AGAINST INV. 95 (SEQ.IDs. 216, 43) ---	1-14, 18, 26-30, 35-38
X	DATABASE EMBL 'Online! Accession Number AA839940, 2 March 1998 (1998-03-02) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:1259911 5' similar to SW:KMLC_RAT P20689 myosin light chain kinase." XP002167891 abstract DOC. AGAINST INV. 55 (SEQ.IDs. 176, 58) ---	1, 2, 4, 6, 7, 10-13, 18
X	DATABASE EMBL 'Online! Accession Number AL031055, 10 July 1998 (1998-07-10) RAMSAY H.: "Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1." XP002167892 abstract DOC. AGAINST INV. 56 (SEQ.IDs. 177, 59) ---	1, 2, 4-7, 10-14, 18
P, X	DATABASE EMBL 'Online! Accession Number AL137662, 27 January 2000 (2000-01-27) KOEHRER K. ET AL.: "Homo sapiens mRNA" XP002167893 abstract DOC. AGAINST INV. 57 (SEQ.IDs. 178, 60) ---	2, 6, 7, 11, 12
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X	<p>NAGASE T. ET AL.: "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro"</p> <p>DNA RESEARCH, vol. 4, no. 4, 28 April 1997 (1997-04-28), pages 141-150, XP002102085 ISSN: 1340-2838 the whole document -& DATABASE EMBL 'Online! Accession Number AB002342, 1 July 1997 (1997-07-01) NAGASE T. ET AL.: "Human mRNA for KIAA0344 gene." XP002167894 abstract DOC. AGAINST INV. 59 (SEQ.IDs. 180, 62)</p>	2,6,7, 11,12
X	<p>WO 98 36054 A (HOOPER JOHN DAVID ;AMRAD OPERATIONS PTY LTD (AU); ANTALIS TONI MAR) 20 August 1998 (1998-08-20) SEQ.IDs. 9 and 10 DOC. AGAINST INV. 60 (SEQ.IDs. 181, 63)</p>	1-14, 26-30, 35-38
X	<p>ANDERSON K. A. ET AL.: "Components of a calmodulin-dependent protein kinase cascade. Molecular cloning, functional characterization and cellular localization of Ca2+/calmodulin-dependent protein kinase kinase beta."</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 48, 27 November 1998 (1998-11-27), pages 31880-31889, XP002167887 ISSN: 0021-9258 the whole document -& DATABASE EMBL 'Online! Accession Number AF140507, 21 May 1999 (1999-05-21) ANDERSON K. A. ET AL.: "Homo sapiens Ca2+/calmodulin-dependent protein kinase beta, complete cds." XP002167895 abstract DOC. AGAINST INV. 62 (SEQ.IDs. 183, 65)</p>	1-14,23, 26,27
P,X	<p>WO 99 58558 A (INCYTE PHARMA INC ;PATTERSON CHANDRA (US); YUE HENRY (US); BANDMAN) 18 November 1999 (1999-11-18) SEQ.IDs. 2 and 15 DOC. AGAINST INV. 62 (SEQ.IDs. 183, 65)</p>	2,6,7,9, 11,12, 26-28
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P,X	US 6 013 455 A (AZIMZAI YALDA ET AL) 11 January 2000 (2000-01-11) SEQ.IDs. 2 and 11 DOC. AGAINST INV. 63 (SEQ.IDs. 184, 66) ---	1-14, 26-30, 35-38
X	EP 0 870 825 A (SMITHKLINE BEECHAM CORP) 14 October 1998 (1998-10-14) figure 2 DOC. AGAINST INV. 65 (SEQ.IDs. 186, 68) DOC. AGAINST INV. 66 (SEQ.IDs. 187, 69) ---	1-14, 25-30, 35-38
X	DATABASE EMBL 'Online! Accession Number AA589241, 18 September 1997 (1997-09-18) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:992145 5' similar to WP:F49E11.1 CE05897 serine/threonine protein kinase." XP002167897 abstract DOC. AGAINST INV. 66 (SEQ.IDs. 187, 69) ---	1,2,4,6, 7,10-13, 25
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X	WO 94 05794 A (MASSACHUSETTS INST TECHNOLOGY) 17 March 1994 (1994-03-17) page 13, paragraph 2 examples 1,2 DOC. AGAINST INV. 68 (SEQ.IDs. 189, 71) ---	1-14, 26-28, 35-38
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X	DATABASE EMBL 'Online! Accession Number AA387681, 25 June 1997 (1997-06-25) MARRA M. ET AL.: "Mus musculus cDNA clone." XP002167898 abstract DOC. AGAINST INV. 70 (SEQ.IDs. 191, 73) ---	6,7
P,X	WO 00 09678 A (TULARIK INC) 24 February 2000 (2000-02-24) the whole document DOC. AGAINST INV. 71 (SEQ.IDs. 192, 74) ---	1-14,20, 26,27, 29,30, 35-38
X	DATABASE EMBL 'Online! Accession Number AF046653, 6 April 1998 (1998-04-06) ZAMBROWICZ B. P. ET AL.: "Mus musculus genomic clone OST10140." XP002167969 abstract DOC. AGAINST INV. 76 (SEQ.IDs. 197, 79) ---	1-4, 6-13,25
P,X	DATABASE EMBL 'Online! Accession Number AF238255, 12 April 2000 (2000-04-12) LIU T. C. ET AL.: "Homo sapiens mixed lineage kinase mRNA." XP002167970 abstract -& LIU T.-C. ET AL.: "Cloning and expression of ZAK, a mixed lineage kinase-like protein containing a leucine-zipper and a sterile-alpha motif." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 274, 11 August 2000 (2000-08-11), pages 811-816, XP002167968 the whole document DOC. AGAINST INV. 77 (SEQ.IDs. 198, 80) ---	1-14
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X	<p>DATABASE EMBL 'Online! Accession Number AA270784, 28 March 1997 (1997-03-28) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:736476." XP002167971 abstract DOC. AGAINST INV. 80 (SEQ.IDs. 201, 83)</p> <p>---</p>	<p>6,7</p>
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X	<p>DATABASE EMBL 'Online! Accession Number AL031297, 13 August 1998 (1998-08-13) COBLEY V.: "Human DNA sequence from clone 97P20 on chromosome1q23.2-24.3." XP002168227 abstract DOC. AGAINST INV. 81 (SEQ.IDs. 202, 84)</p> <p>---</p>	<p>1-14</p>
X	<p>WO 99 04265 A (SAHIN UGUR ;TURECI OZLEM (DE); PFREUNDSCHUH MICHAEL (DE); GOUT IVA) 28 January 1999 (1999-01-28) SEQ.IDs. 431 and 435 DOC. AGAINST INV. 82 (SEQ.IDs. 203, 85)</p> <p>---</p>	<p>2,6,7, 11,12</p>
X	<p>DATABASE EMBL 'Online! Accession Number AA195964, 28 January 1997 (1997-01-28) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:628136" XP002168228 abstract DOC. AGAINST INV. 84 (SEQ.IDs. 205, 87)</p> <p>---</p>	<p>6,7</p>
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X	<p>DATABASE EMBL 'Online! Accession Number AF027406, 6 January 1999 (1999-01-06) BRENNER V. ET AL.: "Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA." XP002168230 abstract DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88)</p>	1-14
X	<p>DATABASE EMBL 'Online! Accession Number AF043288, 6 January 1999 (1999-01-06) BRENNER V. ET AL.: "Mus musculus muscle-specific serine kinase 1 mRNA." XP002168231 abstract DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88)</p>	1-4,6-13
P,X	<p>WO 00 22143 A (INCYTE PHARMA INC ;AZIMZAI YALDA (US); CORLEY NEIL C (US); YUE HEN) 20 April 2000 (2000-04-20) SEQ.IDs. 1 and 10 DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88) SEQ.IDs. 7 and 16 DOC. AGAINST INV. 104 (SEQ.IDs. 225, 107)</p>	1-4, 6-13, 26-28
X	<p>DATABASE EMBL 'Online! Accession Number AI553938, 25 March 1999 (1999-03-25) STAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2090493 3' similar to TR:015367 TSK_1." XP002168388 abstract DOC. AGAINST INV. 86 (SEQ.IDs. 207, 89) DOC. AGAINST INV. 87 (SEQ.IDs. 208, 90) DOC. AGAINST INV. 91 (SEQ.IDs. 212, 94)</p>	1,2,4-7, 10-14,25

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X	<p>DATABASE EMBL 'Online! Accession Number AA399596, 29 April 1997 (1997-04-29) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:729913 5' similar to TR:G404634 Serine/threonine kinase." XP002168766 abstract DOC. AGAINST INV. 88 (SEQ.IDs. 209, 91) ---</p>	1,2,4-7, 10-14,25
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X	<p>DATABASE EMBL 'Online! Accession Number AI652441, 5 May 1999 (1999-05-05) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2307063 3' similar to TR:P97417 serine/threonine kinase" XP002168390 abstract DOC. AGAINST INV. 89 (SEQ.IDs. 210, 92) ---</p>	1,2,4-7, 10-14
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X	DATABASE EMBL 'Online! Accession Number AI606679, 26 April 1999 (1999-04-26) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:516008." XP002169148 abstract DOC. AGAINST INV. 100 (SEQ.IDs. 221, 103) --- -/--	6,7

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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 31-34
because they do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:
see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.: 1-16 (partially), 17 (completely), 18 and 19 (partially), 20 and 22 (completely), 23-38 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A nucleic acid molecule encoding a kinase polypeptide as represented by a 'gene name' selected from 'AA980090', 'AA045601', 'AA297313', 'N23936', '5R72-18-1', '5R79-54-1', '5R65-16-1', 'AA065538', 'H17727', 'W08549', 'AA430250', 'AA139478', 'R87679', 'W65887', 'AA948538', '5R69-23-3', and '5R69-26-2', wherein invention 122 is limited to 'AA980090', invention 123 is limited to 'AA045601', and invention 136 is limited to '5R69-26-2', or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide encoded by said nucleic acid molecule or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a said polypeptide.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 31-34

The search was based on the sequence listing furnished in computer readable form, the numbering of which differs from the numbering in the figures.

Claims 31-34 refer to a 'substance that modulates the activity of a kinase' without giving a true technical characterization. Moreover, no such specific compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

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